

STE20_h	MAH	LRGFANQH	SRV	---	DPEEL	FTKL	DRIGKGSFGEV	YKGI	DNHTK	43										
MST3_h	MAH	SPVQSGLP	GMQNLK	ADPEEL	FTKL	EKIGKGSFGEV	FKGI	DNRTQ	47											
STLK2_h	MAH	SPVAVQVP	GMQNNIA	DPEEL	FTKL	ERIGKGSFGEV	FKGI	DNRTQ	47											
STLK3_h	TAAPAA	PAPAPAPAA	QAQAVGW	PICRDAYELQ	EVI	SGATAVVQAALCKPRQ			57											
STE20_h	EVVAIK	IIDLEAEDE	IEDIQQE	ITVLSQC	DSPI	TRYFGSYLK	STKLWII	MEYLG	100											
MST3_h	KVVAIK	IIDLEAEDE	IEDIQQE	ITVLSQC	DSPI	TKYYGSYLK	DTKLWII	MEYLG	104											
STLK2_h	QVVAIK	IIDLEAEDE	IEDIQQE	ITVLSQC	DSPI	TKYYGSYLK	GSKLWII	MEYLG	104											
STLK3_h	ERVAIK	RINLEK	CQTSMD	ELLKEIQAM	SQCSHPIN	VVTYTSFVVKDELWLV	IMKLLSG		114											
STE20_h	GSALD	LLKPGP	---	LEET	YIA	TILREIL	KGLDY	LHSE	RKIHRD	IKAANVLL	148									
MST3_h	GSALD	LLKPGP	---	LDET	QIA	TILREIL	KGLDY	LHSE	KKIHRD	IKAANVLL	152									
STLK2_h	GSALD	LLRAGP	---	FDEF	QIA	TMLKEIL	KGLDY	LHSE	KKIHRD	IKAANVLL	152									
STLK3_h	GSM	LDII	KYIVNRGE	HKNGVLE	EAA	IIATILKEVL	EGLDY	LHRNGQ	IHRDL	KAGNILL	171									
STLK4_h	---	---	---	KSGV	LDX	STIA	TILREVL	EGL	EY	LHKXGQIHRD	VKAGNILLX	41								
STE20_h	SEQ	GDV	VKL	ADFGV	-A	---	GQL	TD	TQIK	RNTF	VG	TPFW	MAPEV	IKQ	SA	-YDF	KADI	198		
MST3_h	SEHG	EV	VKL	ADFGV	-A	---	GQL	TD	TQIK	RNTF	VG	TPFW	MAPEV	IKQ	SA	-YDS	KADI	202		
STLK2_h	SEQ	GDV	VKL	ADFGV	-A	---	GQL	TD	TQIK	RNTF	VG	TPFW	MAPEV	IKQ	SA	-YDS	KADI	202		
STLK3_h	GED	GSV	QI	ADFGV	SA	FLAT	G	GV	TR	NKV	-R	K	TF	VG	TPC	WMAPEV	MEQ	V	RGM	227
STLK4_h	GED	GSV	QI	ADFGV	SA	FLAT	G	GV	TR	NKV	-R	K	TF	VG	TPC	WMAPEV	MEQ	V	RGM	97

Fig. 1A

Fig. 1B

STE20_h	RQ--PRSQCLSTLVRPVFGELKEKHKQSGGSGVGALEELENAFSLAEESCPGISDKLM	405
MST3_h	IPKRPFSCCLSTIISPLFAELKEKSQACGGNLSIEELRGAIYLAEEACPGISDTMV	411
STLK2_h	-----CLSMIITPAFAELKQQDENNASRNQAIIEELKSI AVAAACPGITDKMV	400
STLK3_h	DY--REASSCAVNVLRLRNSRKELNDIRFEFTPGRDTADGVSSQELFSAGLVDGHDV	468
STLK4_h	-----ISLVLRLRNSKELNDIRFEFTPGRDTAEGVSSQELISAGLVDGRDL	366
STE20_h	VHILVERVQRFSSHNRNHLTSTR	426
MST3_h	AQLVQRLQRYSLSGGGTSSH	431
STLK2_h	KKLIEKFQKCSADESP	416
STLK3_h	VIVAAANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLIGFAQLSVS	516
STLK4_h	VIVAAANLQKIVEEPQSNR[VTFKLASGVEGSDIPDDGKLIGFAQLSIS	414

Fig. 1C

Ste20_h	MAHLRGFANQHSRV	----	DPEELFTKLDRI	IGKGSFGE	VYK	GIDNHTK	43	
T19A5.2_ce	MTTSSDELPRQADD	SMKWDRIYIQKLD	PEVIFTKQERIG	SGFGE	VYK	GIDNRTG	57	
Pak_sp	-----	-----	LLYRNFVKIG	QSG	VDVY	SARQVGIN	26	
STLK5_h	-----	-----	-----	-----	-----	-----	0	
Ste20_h	EVVAIKIIDLEEA	EDEIEDIQQEIT	VLSQCDSPI	TRYFGSYLK	STKLWI	IIMEYLG	100	
T19A5.2_ce	RVVAIKIIDLEQA	EDEIEDIQQEIQ	VLSQCDSQY	VTKYFGSFL	KSKLWI	IIMEYLG	114	
Pak_sp	LSVAIKKMNINQ	QPKKEF-IVNEI	LVMSKSHHKN	IVNFIDTFF	YKSELWM	VMEYMRG	82	
STLK5_h	-----	-----	-----	-----	-----	-----	0	
Ste20_h	GSALDLLKPGPI	EETYYIA	TILREI	LKGLDIY	LHSE	KIHRDIK	ANVL	157
T19A5.2_ce	GSALDLTKSGKL	DESHIAVIL	REILKGL	EYLVHSE	KIHRDIK	ANVL	171	
Pak_sp	GSILTEVV	TNNTLSE	QIAAICKET	LEGLQLH	LHENGIV	HRDIKSDN	IL	139
STLK5_h	--LIC	THFMDGMNEL	AIAYIL	QGVLLK	ALDIYI	IHHMGYV	HRSVKASHIL	55
Ste20_h	DFGVAGQL	TDTIKRN	TFVGT	PF--	WMAPEV	IKQSA--	YDFKA	205
T19A5.2_ce	DFGVAGQL	TETVKKR	ITFVG	SPF--	WMAPEL	IKQSS--	YDYKA	219
Pak_sp	DFGFCAQ	IDSNMTKR	TTIMV	GTPIY--	WMAPEV	VTRKE--	YGFKV	187
STLK5_h	GLRSNLS	MISAGQRQR	VVHDF	PKYSVKVLP	WLSPEV	LQQLN	QGYDAKSDI	112
Ste20_h	IELAKGEPP	NSDLHP	MRVLF	FLIPK-NS	PPTL	LEG-Q--	-----	238
T19A5.2_ce	IELANGEP	PHSDLHP	MRVLF	FLIPK-NP	PPVL	QGSQ--	-----	253
Pak_sp	IELMVEGE	PPYLNENP	LRALYL	IA	TIGTPK	ISRPEL--	-----	222
STLK5_h	IELANGHVP	FKDMPATQM	LLEKLN-G	TVPC	LLD-T	STIPAEEL	TMSPSR	167

Fig. 2A

Fig. 2B

ZC504.4_ce	MSSSGEDE---	IDLNSLRDPAGIFEL	IEVVGNGTYGQVYK	GRHVKT	AQLAAIKIMNINE	58
NIK_m	MANDSPAKSLVDIDL	SSLRDPAGIFEL	VEVVGNGTYGQVYK	GRHVKT	VT-AAIKVMDVTE	69
ZC1_h	MANDSPAKSLVDIDL	SSLRDPAGIFEL	VEVVGNGTYGQVYK	GRHVKT	GQLAAIKVMDVTE	60
ZC2_h	-----	-----	AFGEVYEGRHKVTGQLAAIKVMDVTG			28
ZC3_h	-----	-----	AFGEVYEGRHKVTGQLAAIKVMDVTE			28
ZC504.4_ce	DEEIDEIKLEINMLKK	HSHHRNVATYYGAFIKKL	PSSTGKH	DQLWLVMFCG	SGSITDLVK	116
NIK_m	DEEEETLEINMLKKYSHHRN	IATYYGAFIKKSPPGHD		DQLWLVMFCG	SGSITDLVK	117
ZC1_h	DEEEIKLEINMLKKYSHHRN	IATYYGAFIKKSPPGHD		DQLWLVMFCG	SGSITDLVK	118
ZC2_h	DEEEIKQLEINMLKKYSHHRN	IATYYGAFIKKSPPGMD		DQLWLVMFCG	SGSITDLIK	84
ZC3_h	DEEEIKQLEINMLKKYSHHRN	IATYYGAFIKKSPPGND		DQLWLVMFCG	SGSITDLVK	84
ZC504.4_ce	NTKGGSLLKEE	WIAIYICREILRGLYHLHQ	SKVIHRDIKQNVLLT	DSAEVKLVD	FGVSAQL	176
NIK_m	NTKGNTLLKEDWIAIYI	SREILRGLAHLHI	HHV IHRDIKQNVLLT	TENAEVKLVD	FGVSAQL	177
ZC1_h	NTKGNTLLKEDWIAIYI	SREILRGLAHLHI	HHV IHRDIKQNVLLT	TENAEVKLVD	FGVSAQL	178
ZC2_h	NTKGNTLLKEE	WIAIYICREILRGLSHLHQ	HKV IHRDIKQNVLLT	TENAEVKLVD	FGVSAQL	144
ZC3_h	NTKGNA	LLKEDCIAIYICREILRGLAHLHA	HKV IHRDIKQNVLLT	TENAEVKLVD	FGVSAQL	144
ZC504.4_ce	DKTVGRRNTFIGTPYWM	APVEIACDESP	EATYDSRSDLSL	GITAL	EMAEGHPPLCDMHP	236
NIK_m	DRTVGRRNTFIGTPYWM	APVEIACDENPD	ATYDYSRDLWS	CGITAI	EMAEGGPPPLCDMHP	237
ZC1_h	DRTVGRRNTFIGTPYWM	APVEIACDENPD	ATYDYSRDLWS	CGITAI	EMAEGAPPLCDMHP	238
ZC2_h	DRTVGRRNTFIGTPYWM	APVEIACDENPD	ATYDFKSDLSL	GITAI	EMAEGAPPLCDMHP	204
ZC3_h	DRTVGRRNTFIGTPYWM	APVEIACDENPD	ATYDYSRDT	WLSLGITAI	EMAEGAPPLCDMHP	204

Fig. 3A

ZC504.4_ce	MRALFLIPRNPPPPKILKRNNKKWTKKKFTFIEITVLVKIDYHQRPYTGALLRHHPFFIKEQPHEQT	296
NIK_m	MRALFLIPRNPPPPRLK-SKKWSKKFFSFIEGCLVKKNYMQRPSTEQLLKHFFIRDQPNERQ	296
ZC1_h	MRALFLIPRNPPPPRLK-SKKWSKKFFSFIEGCLVKKNYMQRPSTEQLLKHFFIRDQPNERQ	297
ZC2_h	MRALFLIPRNPPAPRLK-SKKWSKKFFSFIESCLVKKNHSQRPATTEQLMKHHPFIRDQPNERQ	263
ZC3_h	MRALFLIPRNPPPPRLK-SKKWSKKFTDFIDTCLIKTYLSRPPTEQLLKFPPFIRDQPTTERQ	263
ZC504.4_ce	IRHSIKEIHIDRNRVRKKQDADYEYSGSEDDIEPSPNNRRDSESS--SMIPMDNTLRKGFQ	353
NIK_m	VRIQLKDHIDRTRKKRGEKDETEYEYSGSEEEEEVEPEQEGEPSSIVNVPGESTLRRDFL	356
ZC1_h	VRIQLKDHIDRTRKKRGEKDETEYEYSGSEEEEEVEPEQEGEPSSIVNVPGESTLRRDFL	357
ZC2_h	VRIQLKDHIDRTRKKRGEKDETEYEYSGSEEEEEVEPEQEGEPSSIVNVPGESTLRRDFL	321
ZC3_h	VRIQLKDHIDRTRKKRGEKEETEYEYSGS-EEEDDSHGEEGEPSSIMNVPGESTLRRDFL	322
ZC504.4_ce	KLQESSRGFAEPGAQQLLRRLPQQPAPAPFYQQSRYVEPRRESSSEVKLRAVSSRGAADGP	413
NIK_m	RLQQENKSEALRRQQLLQEQQL-----REQEEYKQQLLAERQKRI--	398
ZC1_h	RLQQENKSEALRRQQLLQEQQL-----REQEEYKQQLLAERQKRI--	399
ZC2_h	RLQLANKERSEALRRQQLLQEQQL-----RENEEHKQQLLAERQKRI--	361
ZC3_h	RLQQENKSNSEALKQQQQLLQQQQQ-----RQPEAHIKHLHQRRRI--	364
ZC504.4_ce	RHSPASRRPRPRSPQQSHPAAPHLADLANYEKRRRSEREEERRERERQAHHAMPIARVSA SV	473
NIK_m	EEQKEQRRRLEEQQRRREAREARRQQEREQRRRIEEKRRLEELERRRKEEEERRRRAEEEEKR	458
ZC1_h	EEQKEQRRRLEEQQRRREAREARRQQEREQRRRIEEKRRLEELERRRKEEEERRRRAEEEEKR	459
ZC2_h	EEQKEQRRRLEEQQRRREKELRKQQRREHYEEQMR-----EEEEER	404
ZC3_h	EEQKFERRRVVEEQQRREERQKLQEKEQRRLEDMQAL-----RREER	409

Fig. 3B

ZC504.4_ce	PAPQQSRKMSEPLILITHVKPELDLVLASELSKMG	508
NIK_m	RVEREQEYIRRRQLLEEEQRHLETLQQQLLQEAMLL	493
ZC1_h	RVEREQEYIRRRQLLEEEQRHLEVLQQQLLQEAMLL	519
ZC2_h	RAEHQEQYKRRKQLEEQ	435
ZC3_h	QAREEQEYIRHRLEEEQRQLEILQQQLLQEALLL	469
ZC504.4_ce	HHNGRRSREES-MSPPPPAPPPPREASISSITDIDVGELDNGAQAEWDDLKDIMM	561
NIK_m	HDHRRIPHAQ-QQPPPPQQQDRSKPSFHAPFEPKPHYDPADRAREVQWSHLASLKN	548
ZC1_h	YLLSLQHDHRRIPHPQHSSQPPPPQQQERSKPSFHAPFEPKAHYEPADRAREVEDRFRKTNHS	579
ZC2_h	YLLVSLQHQR	484
ZC3_h	YLLKSLQQQQQQLQK-QQQQQQLLPQDRKPLHYHGRGMNPADKPAWAREVERTRMKNKQQ	528
ZC504.4_ce	NGEGTLRG	595
NIK_m	NYSPVSRSHSFSDPSPKFAHHHLRSQDPCPPSRSEGLSQSSDSKSEVPPEPTQK	599
ZC1_h	SPEAQSKQ	620
ZC2_h	SPAMPHKV	531
ZC3_h	NSPLAKSK	574
ZC504.4_ce		595
NIK_m		599
ZC1_h		620
ZC2_h	LVAVKSQGPALTASQSV	575
ZC3_h	KSLVAHRVPLKPYAAPVPRSQSLQDQDQPTRNLAAFPASHDPDAIPAPTATPSARGAVIRQ	634

Fig. 3C

ZC504.4_ce 755
EGADDS TSGPEDTRAASSPNLSNGETESVKTMIVHDDVSEEPAMTP--SKEGTLIV-- 831
EGADES TSGPEDTRAASSNLNSNGETESVKTMIVHDDVSEEPAMTP--SKEGTLIV-- 837
ETHDGTVAVSDIPRLIPTGAPGSNEQYNVGMVGTHTGLETSHADSFSGISREGTLMIRET 845
GPAEGS--RDTPGGRDGDTSVSTMVVHDVEEITGTQPP--YGGGTMVVQRT 885

ZC504.4_ce 755
NIK_m--RQTQSA SSTLQKHK 845
ZC1_h--RRTQSA SSTLQKHK 851
ZC2_hSGEKRS GHSNGFAGHINLPDLVQQSHSPAGTPTTEGLGRVSTHSQEMDSSGTEYGMGSS 905
ZC3_hPEEERNLLHADSNGYT--NLPDVVQPSHSPTENSKGQSPPSKDGSDYQSRGLVKAPG- 941

ZC504.4_ce 772
SSSFTPFIDPRLLQIISPS SGTTVTSVVGFS CDGLRPEAIRQDPT--NQVQVNVTPNSN 901
SSSFTPFIDPRLLQIISPS SGTTVTSVVGFS CDGMRPEAIRQDPT--RKGSVNVNPT 907
TKASFTPFVDP RVYQTSP TDEDEEDESAAALFTGELLRQEAKLNEARKISVNVNPT 965
-KSSFTMFVDLGIYQPGGSGDSIPITALVGGEGTRLDQLQYDV--RKGSVNVNPT 994
ZC4_h--NVNPL 5

ZC504.4_ce 832
GTPAENDAP EIRKYKKKFSGEILCAALWGVNLLIGTDSGLMLLDRSGQGKVPYPLISRRRF 832
NTRPQSDTPEIRKYKKRFNSEILCAALWGVNLLVGTESGLMLLDRSGQGKVPYPLISRRRF 961
NTRPQSDTPEIRKYKKRFNSEILCAALWGVNLLVGTESGLMLLDRSGQGKVPYPLINRRRF 967
NIRPHSDTPEIRKYKKRFNSEILCAALWGVNLLVGTENGLMLLDRSGQGKYYNLIINRRRF 1025
NTRAHS ETPEIRKYKKRFNSEILCAALWGVNLLVGTENGLMLLDRSGQGKYYGLIGRRRF 1054
YVSPACKKPLIHMYEKEFTSEICCGSLWGVNLLIGTRSNLYLMDRSGKADITKLI RRRPF 65

Fig. 3E

ZC504.4_ce	DQM	TV	LEG	Q	N	I	L	A	T	I	S	G	R	K	R	R	I	R	V	Y	Y	L	S	W	L	R	Q	K	I	L	R	T	E	G	A	G	S	A	N	T	T	E	K	R	N	G	W	V	N	V	G	D	--	889						
NIK_m	QQ	MD	V	LEG	N	V	L	V	T	I	S	G	K	K	D	K	L	R	V	Y	Y	L	S	W	L	R	N	K	I	L	H	N	D	P	E	V	--	--	--	--	--	--	--	--	--	--	--	--	--	1013										
ZC1_h	QQ	MD	V	LEG	N	V	L	V	T	I	S	G	K	K	D	K	L	R	V	Y	Y	L	S	W	L	R	N	K	I	L	H	N	D	P	E	V	--	--	--	--	--	--	--	--	--	--	--	--	1019											
ZC2_h	QQ	MD	V	LEG	N	V	L	V	T	I	S	G	K	K	N	K	L	R	V	Y	Y	L	S	W	L	R	N	R	I	L	H	N	D	P	E	V	--	--	--	--	--	--	--	--	--	--	--	--	1077											
ZC3_h	QQ	MD	V	LEG	N	V	L	V	T	I	S	G	K	R	N	K	L	R	V	Y	Y	L	S	W	L	R	N	K	I	L	H	N	D	P	E	V	--	--	--	--	--	--	--	--	--	--	--	--	1106											
ZC4_h	RQ	L	Q	V	L	E	P	L	N	L	I	T	I	S	G	H	K	N	R	L	R	V	Y	H	L	T	W	L	R	N	K	I	L	N	D	P	E	S	--	--	--	--	--	--	--	--	--	--	--	120										
ZC504.4_ce	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	944												
NIK_m	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1068												
ZC1_h	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1074												
ZC2_h	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1132												
ZC3_h	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1161												
ZC4_h	KA	ID	K	L	T	G	C	E	H	F	S	V	L	Q	H	E	T	T	Y	I	A	I	A	L	K	S	S	I	H	L	Y	A	W	A	P	K	S	F	D	E	S	T	A	I	K	V	E	P	T	L	D	H	K	P	V	T	V	180		
ZC504.4_ce	DL	T	V	E	D	N	A	R	L	K	V	L	Y	G	S	T	G	F	H	A	I	D	L	D	S	A	A	V	Y	D	I	Y	T	P	A	Q	S	G	Q	T	T	I	P	H	C	I	V	V	L	P	N	S	N	G	M	Q	L	L	1004	
NIK_m	DL	T	V	E	E	G	Q	R	L	K	V	I	Y	G	S	C	A	G	F	H	A	V	D	V	D	S	G	S	V	Y	D	I	Y	L	P	T	H	I	Q	C	S	I	K	P	H	A	I	I	L	P	N	T	D	G	M	E	L	L	1128	
ZC1_h	DL	T	V	E	E	G	Q	R	L	K	V	I	Y	G	S	C	A	G	F	H	A	V	D	V	D	S	G	S	V	Y	D	I	Y	L	P	T	H	I	Q	C	S	I	K	P	H	A	I	I	L	P	N	T	D	G	M	E	L	L	1134	
ZC2_h	DL	T	V	E	E	G	Q	R	L	K	V	I	F	G	S	T	G	F	H	V	I	D	V	D	S	G	N	S	Y	D	I	Y	T	P	S	H	I	Q	G	N	I	T	P	H	A	I	V	I	L	P	K	T	D	G	M	E	M	L	1192	
ZC3_h	DL	T	V	E	E	G	Q	R	L	K	V	I	Y	G	S	S	A	G	F	H	A	V	D	V	D	S	G	N	S	Y	D	I	Y	I	P	V	H	I	Q	S	Q	I	T	P	H	A	I	I	F	L	P	N	T	D	G	M	E	M	L	1221
ZC4_h	DL	I	A	I	G	S	E	K	R	L	K	I	F	F	S	S	A	D	G	Y	H	L	I	D	A	E	S	E	V	M	S	D	V	T	L	P	K	N	P	L	E	I	I	I	P	Q	N	I	I	L	P	D	C	L	G	I	G	M	M	240

Fig. 3F

ZC504.4_ce
NIK_m
ZC1_h
ZC2_h
ZC3_h
ZC4_h

L	C	Y	D	N	E	G	V	Y	V	N	T	Y	G	R	M	T	K	N	V	V	L	Q	W	G	E	M	P	S	S	V	A	Y	I	S	T	G	Q	I	M	G	W	G	N	K	A	I	E	I	R	S	V	D	T	G	H	L	D	G	V
V	C	Y	E	D	E	G	V	Y	V	N	T	Y	G	R	I	T	K	D	V	V	L	Q	W	G	E	M	P	T	S	V	A	Y	I	R	S	N	Q	T	M	G	W	G	E	K	A	I	E	I	R	S	V	E	T	G	H	L	D	G	V
V	C	Y	E	D	E	G	V	Y	V	N	T	Y	G	R	I	T	K	D	V	V	L	Q	W	G	E	M	P	T	S	V	A	Y	I	R	S	N	Q	T	M	G	W	G	E	K	A	I	E	I	R	S	V	E	T	G	H	L	D	G	V
V	C	Y	E	D	E	G	V	Y	V	N	T	Y	G	R	I	T	K	D	V	V	L	Q	W	G	E	M	P	T	S	V	A	Y	I	H	S	N	Q	I	M	G	W	G	E	K	A	I	E	I	R	S	V	E	T	G	H	L	D	G	V
L	C	Y	E	D	E	G	V	Y	V	N	T	Y	G	R	I	T	K	D	V	V	L	Q	W	G	E	M	P	T	S	V	A	Y	I	C	S	N	Q	I	M	G	W	G	E	K	A	I	E	I	R	S	V	E	T	G	H	L	D	G	V
L	T	F	N	A	E	A	L	S	V	E	A	N	E	Q	L	F	K	K	I	L	E	M	W	K	D	I	P	S	S	I	A	F	E	C	T	D	R	T	T	G	W	G	Q	K	A	I	E	V	R	S	L	Q	S	R	V	L	E	S	E

ZC504.4_ce
NIK_m
ZC1_h
ZC2_h
ZC3_h
ZC4_h

F	M	H	K	K	A	Q	K	L	K	F	L	C	E	R	N	D	K	V	F	F	S	A	K	G	G	S	C	Q	I	I	Y	F	M	T	L	N	K	P	G	L	T	N	W				
F	M	H	K	R	A	Q	R	L	K	F	L	C	G	R	N	D	K	V	F	F	S	S	V	R	S	G	G	S	S	Q	V	Y	F	M	T	L	G	R	T	S	L	L	S	W			
F	M	H	K	R	A	Q	R	L	K	F	L	C	E	R	N	D	K	V	F	F	A	S	V	R	S	G	G	S	S	Q	V	Y	F	M	T	L	G	R	T	S	L	L	S	W			
F	M	H	K	R	A	Q	R	L	K	F	L	C	E	R	N	D	K	V	F	F	A	S	V	R	S	G	G	S	S	Q	V	F	F	M	T	L	N	R	N	S	M	M	N	W			
F	M	H	K	R	A	Q	R	L	K	F	L	C	E	R	N	D	K	V	F	F	A	S	V	R	S	G	G	S	S	Q	V	Y	F	M	T	L	N	R	I	M	N	W					
L	K	R	R	S	I	K	K	L	R	F	L	C	T	R	G	D	K	L	E	F	T	S	T	L	R	N	H	S	R	V	Y	F	M	T	L	G	K	L	E	E	L	Q	S	N	Y	D	V

Fig. 3G


```

* . . . * .
KHS1_h 362 -SDPNFMLQWNP-----FV-----D 375
KHS2_h 359 LDSSEEIYYTARSNLDLQLEYGQGHGQGYFLGANKSLLKSVEEELHQRGHVAHLEDEGD 418

* . . . * .
KHS1_h 376 GANTGKSTSKRAIPPLPKPRISSYPED-NFPDEEKASTIKHCP--DSESRAPIILRRQ 432
KHS2_h 419 DDESKHSTLKAKIPPLPKPKSIFIPQEMHSTEDENQGTIKRCPMMSGSPAKPSQVPPRP 478

* . . . * .
KHS1_h 433 SSPSCGPVAETSSIGNGDGISKL-MSENTEGSA-----QAPQLPRKNDKRDFFPKPAIN 484
KHS2_h 479 PPRP--LPPHKPVALGNMGMSFQLMGERDGSQCQQQNEHRGTNLSRK-EKKDVPKPISN 534

* . . . * .
KHS1_h 485 GLPPTPKVLMGACFSKVFDGCPKINCATSWIHPDTKDQYIIFGTEDGIYTLNLNELHEA 544
KHS2_h 535 GLPPTPKVHMGACFSKVFNCGCPKIHCASSWINPDTRDQYLIFGAEEGIYTLNLNELHET 594

* . . . * .
KHS1_h 545 TMEQLFPRKCTWLYVINNTLMSLSEKTFQLYSHNLIALFEHAK-KPGLAAHIQTHRFPD 603
KHS2_h 595 SMEQLFPRRCTWLYVMNCLLSIS-GKASQLYSHNLPGLFDYARQMQLPVAIPAHLPD 653

* . . . * .
KHS1_h 604 RILPRKFALTITKIPDTKGCHKCCIVRNPNPYTGHKYLCGALQSGIVLLQWYEPMQKFMLIKH 663
KHS2_h 654 RILPRKFSVSAKIPETKWCQKCCVVRNPNPYTGHKYLCGALQTSIVLLEWVEPMQKFMLIKH 713

```

Fig. 4B

15/76

SULU_ce	L I Q R T K N M V L E L D N F Q Y K K M R K L I M Y L D E T E G K E G S E G N G A S D D L D F H G N E A N S I G R A G D S	360
SULU1_h	L I Q R T K D A V R E L D N L Q Y R K M K K I L F - - - - -	313
SULU3_m	L I Q R T K D A V R E L D N L Q Y R K M K K L L F - - - - -	309
SULU3_h	L I Q R T K D A V R E L D N L Q Y R K M K K L L F - - - - -	103

Fig. 5A

SULU_ce ASSRSASLT SFRSMQSSGGAGLLVSTNTTGAMDNVHGSSGYNGSSSTSSARRRRPPIPS 420
SULU1_h ----- QETRNGLNE S 324
SULU3_m ----- QEAHNGPAVEA 320
SULU3_h ----- QEAHNGPAVEA 114

SULU_ce QMLSSSTSTSGVG T M P S H G S V G A S I T A I A V N P T P S P S E P I P T S Q P T S K S E S S - S I L E T A H D 479
SULU1_h Q E D E E D S E H G T S L N R E M D S L G S N H S I P S M S V S T G S Q S S S V N S M Q E V M D E S S E L V M M H D D 384
SULU3_m Q E E E E E Q D H G V G R T G T V N S V G S N Q S I P S M S I S A S S Q S S S V N S L P D A S D D K S - E L D M M E G D 379
SULU3_h Q E E E E E Q D H G V G R T G T V N S V G S N Q S I P S M S I S A S S Q S S S V N S L P D V S D D K S - E L D M M E G D 173

SULU_ce D P L D T S I ----- R A P V K D L H M P H R A V K E R I A T L Q N H K F A T L R S Q R I I 521
SULU1_h E S T I N S S S V V H K K D H V F T R D E A G H G D P R P E P R P T Q S V Q S Q A L H Y R N R E R F A T I K S A S L V 444
SULU3_m H T V M S N S S V I H L K P E E E N Y Q E E G D P R T R A S D P Q S P P Q V S R H K S H Y R N R E H F A T I R T A S L V 439
SULU3_h H T V M S N S S V I H L K P E E E N Y R E E G D P R T R A S D P Q S P P Q V S R H K S H Y R N R E H F A T I R T A S L V 233

SULU_ce N Q E Q E E Y T K E N N M Y E Q M S K Y K H L R Q A H H K E L Q Q F E R C A L D R E Q L R V K M D R E L E Q L T T T Y 581
SULU1_h T R Q I H E H E Q E N E L R E Q M S G Y K R M R R Q H Q K Q L I A L E N K L K A E M D E H R L K L Q K E V E T H A N N S 504
SULU3_m T R Q M Q E H E Q D S E L R E Q M S G Y K R M R R Q H Q K Q L M T L E N K L K A E M D E H R L R L D K D L E T Q R N N F 499
SULU3_h T R Q M Q E H E Q D S E L R E Q M S G Y K R M R R Q H Q K Q L M T L E N K L K A E M D E H R L R L D K D L E T C R N N F 293

SULU_ce S K E K M R V R C S Q N N E L D K R K K D I E D G E K K M K K T K N S Q N Q Q Q M K L Y S A Q Q L K E Y K Y N K E A Q K 641
SULU1_h S I E L E K L A K K Q V A I I E K E A K V A A D E K K F Q Q Q I L A Q Q K K D L T T F L E S Q K K Q Y K I C K E K I K 564
SULU3_m A A E M E K L I K K H Q A A M E K E A K V M A N E E K K F Q Q H I I Q A Q Q K K E L N S F L E S Q K R E Y K L R K E Q L K 559
SULU3_h A A E M E K L I K K H Q A A M E K E A K V M S N E E K K F Q Q H I I Q A Q Q K K E L N S F L E S Q K R E Y K L R K E Q L K 353

Fig. 5B

SULU_ce	TR	L	R	S	L	N	M	-	P	R	S	T	Y	E	N	A	M	K	E	V	K	A	D	L	N	R	V	K	D	A	R	E	N	D	F	D	E	K	L	R	A	E	L	E	D	E	I	V	R	Y	R	R	Q	Q	L	S	N	L	H	700		
SULU1_h	E	E	M	N	E	D	H	S	T	P	K	K	E	K	Q	E	R	I	S	K	H	K	E	N	L	Q	H	T	Q	A	E	E	E	A	H	L	L	T	Q	Q	R	L	Y	Y	D	K	N	C	R	F	F	K	R	K	I	M	I	K	R	H	624	
SULU3_m	E	E	L	N	E	N	Q	S	T	P	K	K	E	K	Q	E	W	L	S	K	Q	K	E	N	I	Q	H	F	Q	A	E	E	E	A	N	L	L	R	R	Q	Q	Y	L	E	L	E	C	R	R	F	K	R	M	L	L	G	R	H	619			
SULU3_h	E	E	L	N	E	N	Q	S	T	P	K	K	E	K	Q	E	W	L	S	K	Q	K	E	N	I	Q	H	F	Q	A	E	E	E	A	N	L	L	R	R	Q	Q	Y	L	E	L	E	C	R	R	F	K	R	M	L	L	G	R	H	413			
SULU_ce	Q	L	E	E	Q	L	D	D	E	D	V	N	V	Q	E	R	Q	M	D	T	R	H	G	L	L	S	K	Q	H	E	M	T	R	D	L	E	I	Q	H	L	N	E	L	H	A	M	K	K	R	H	L	E	T	Q	H	E	A	E	S	A	760	
SULU1_h	E	V	E	Q	Q	N	I	R	E	E	L	N	K	K	R	T	Q	K	E	M	E	H	A	M	L	I	R	H	D	E	S	T	R	E	L	E	Y	R	Q	L	H	T	L	Q	K	L	R	M	D	L	I	R	L	Q	H	Q	T	E	L	E	684	
SULU3_m	N	L	E	Q	D	L	V	R	E	E	L	N	K	K	R	Q	T	Q	K	D	L	E	H	A	M	L	L	R	Q	H	E	S	M	Q	E	L	E	F	R	H	L	N	T	I	Q	K	M	R	C	E	L	I	R	L	Q	H	Q	T	E	L	T	679
SULU3_h	N	L	E	Q	D	L	V	R	E	E	L	N	K	K	R	Q	T	Q	K	D	L	E	H	A	M	L	L	R	Q	H	E	S	M	Q	E	L	E	F	R	H	L	N	T	I	Q	K	M	R	C	E	L	I	R	L	Q	H	Q	T	E	L	T	473
SULU_ce	S	Q	N	E	Y	T	Q	R	Q	Q	D	E	L	R	K	K	H	A	M	Q	S	R	Q	P	R	D	L	K	I	Q	E	A	Q	I	R	K	Q	Y	R	Q	V	V	K	T	Q	T	R	Q	F	K	L	Y	L	T	Q	M	V	Q	V	820		
SULU1_h	N	Q	L	E	Y	N	K	R	R	E	R	E	L	H	R	K	H	V	M	G	L	R	Q	P	K	N	L	K	A	M	E	M	Q	I	K	K	Q	F	Q	D	T	C	K	V	Q	T	K	Q	Y	K	A	L	K	N	H	Q	L	E	V	744		
SULU3_m	N	Q	L	E	Y	N	K	R	R	E	R	E	L	R	R	K	H	V	M	E	V	R	Q	P	K	S	L	K	S	K	E	L	Q	I	K	K	Q	F	Q	D	T	C	K	I	Q	T	R	Q	Y	K	A	L	R	N	H	L	E	T	739			
SULU3_h	N	Q	L	E	Y	N	K	R	R	E	R	E	L	R	R	K	H	V	M	E	V	R	Q	P	K	S	L	K	S	K	E	L	Q	I	K	K	Q	F	Q	D	T	C	K	I	Q	T	R	Q	Y	K	A	L	R	N	H	L	E	T	533			
SULU_ce	V	P	K	D	E	Q	K	E	L	T	S	R	L	K	Q	D	Q	M	Q	K	V	A	L	L	A	S	Q	Y	E	S	Q	I	K	K	M	V	Q	D	K	T	V	K	L	E	S	W	Q	E	D	E	Q	R	V	L	S	E	K	L	E	K	880	
SULU1_h	T	P	K	N	E	H	K	T	I	L	K	T	L	K	D	E	Q	T	R	K	L	A	I	L	A	E	Q	Y	E	Q	S	I	N	E	M	M	A	S	Q	A	L	R	L	D	E	A	Q	E	A	E	C	Q	A	L	R	L	Q	L	Q	Q	804	
SULU3_m	T	P	K	N	E	H	K	A	I	748																																																				
SULU3_h	T	P	K	S	E	H	K	A	V	L	K	R	L	K	E	E	Q	T	R	K	L	A	I	L	A	E	Q	Y	D	H	S	I	N	E	M	L	S	T	Q	A	L	R	L	D	E	A	Q	E	A	E	C	Q	V	L	K	M	Q	L	Q	Q	593	
SULU_ce	E	L	E	E	L	I	A	Y	Q	K	K	T	R	A	T	L	E	E	Q	I	K	K	E	R	T	A	L	E	E	R	I	G	T	R	R	A	M	L	E	Q	K	I	I	E	E	R	E	Q	M	G	E	M	R	R	L	K	K	E	Q	I	940	
SULU1_h	E	M	E	L	L	N	A	Y	Q	S	K	I	K	M	Q	T	E	A	Q	H	E	R	E	L	Q	K	L	E	Q	R	V	S	L	R	R	A	H	L	E	Q	K	I	E	E	E	L	A	A	L	Q	K	E	R	S	E	R	I	K	N	L	864	
SULU3_h	E	L	E	L	L	N	A	Y	Q	S	K	I	K	M	Q	A	E	A	Q	H	D	R	E	L	R	E	L	E	Q	R	V	S	L	R	R	A	L	L	E	Q	K	I	E	E	E	M	L	A	L	Q	N	E	R	I	R	S	L	653				

Fig. 5C

SULU_ce RDRHSQERHRLLENHFVRRTGSTSRSSGGIAPGVGNSSSIQMAM 982
SULU1_h LERQEREIETFDMESLRLMGFGNLTLDLPKEDYR 898
SULU3_h LERQAREIEAFDSESMRLGFSNMVLSNLSPEAFSHSYPGASGWSHNPTGGPGPHWGHPMG 713

SULU3_h GPPQAWGHPMQGGPPQWGHPSGPMQGVPRGSSMGVRNSPQALRRRTASGGRTEQGMSRSTS 773

SULU3_h VTSQISNGSHMSYT 787

Fig. 5D

```
*****
1 MAFANFRRIILRLSTFEKRKSREYEHVRRDLDPNDVWEIVGELGDGAFGKVYKAKNKETGA 60
1 MAFANFRRIILRLSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVYKAKNKETGA 60

*****
61 LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYYDGKLIWIMIEFCPGGAVDA 120
61 LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYHDGKLIWIMIEFCPGGAVDA 120

*****
121 IMLELDRGLTEPQIQVVCQMLEALNFLHGKRIIHRDLKAGNVLMTLEGDIRLADFGVSA 180
121 IMLELDRGLTEPQIQVVCQMLEALNFLHRSKRIIHRDLKAGNVLMTLEGDIRLADFGVSA 180

*****
181 KNLKTLQKRDSFIGTPYWMAPEVVLCEETMKDAPYDYKADIWSLGITLIEMAQIEPPHHEL 240
181 KNLKTLQKRDSFIGTPYWMAPEVVMCEETMKDTPYDYKADIWSLGITLIEMAQIEPPHHEL 240

*****
241 NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLQHPFVSRVTSN 300
241 NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLEHPFVSSITSN 300

*****
301 KALRELVAEAKAEVMEEIEDGREDEEEDAVDAVPLVNHTQDSANVTQPSLDSNKLQD 360
301 KALRELVAEAKAEVMEEIEDGREDEEEDAVDAASTLENHTQNSSEVSPPSLNADKPLEE 360
```

Fig. 6A

LOK_m 361 S-STPLPPSQPEPVNGPCSQPSGDGGLQTTSPADGLSKNDNDLKVPVPLRKSRPLSMDA 419
GEK2_h 361 SPSTPLAPSQSQDSVNEPCSQPSGDRSLQTTSPVAVPGNENGLAVPPLRKSRPVSM DA 420

LOK_m 420 RIQMDEEKQIPDQDENPSPAASKSQKANQSRPNSSALETLGGEALTNGGLELPSSVTPSH 479
GEK2_h 421 RIQVAQEKQVAEQGGDLSPAANRSQKASQSRPNSSALETLGGEKLANGSLEPPAQAAPGP 480

LOK_m 480 SKRASDCSNLSTSESMDYGTSLSADLSLNKETGSLSLKGSKLHNKTLKRTRRFVVDGVEV 539
GEK2_h 481 SKRDSDCSSLCTSESMDYGTNLSTDLNLKEMGSLSIKDPKLYKTKLKRTRKFVVDGVEV 540

LOK_m 540 SITTSKIISEDEKKDEEMRFLRRQELRELRLQKEEHRNQTQLSSKHELQLEQMHRFEQ 599
GEK2_h 541 SITTSKIISEDEKKDEEMRFLRRQELRELRLQKEEHRNQTQLSNKHELQLEQMHRFEQ 600

LOK_m 600 EINAKKKFYDVELENLERQQQVEKMEQDHSVRRKEEAKRIRLEQDRDYAKFQEQLKQM 659
GEK2_h 601 EINAKKKFFDTELENLERQQQVEKMEQDHAVRRREEARRIRLEQDRDYTRFQEQLKLM 660

LOK_m 660 KKEVKSEVEKLPQQRKESMKQKMEEHSQKKQLDRDFVAKQKEDLELAMRKLTTENRRE 719
GEK2_h 661 KKEVKNEVEKLPQQRKESMKQKMEEHTQKKQLDRDFVAKQKEDLELAMKRLTTDNRRRE 720

```

*****
720 ICDKERDCLSKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQQRHDLRLKHEKE 779
721 ICDKERECLMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQQRHELLRLKHEKE 780

*****
780 REQMQRYNQRMMEQLKVRQQQEKKARLPKIQRSDGETRMAMYKKSLHINGAGSASEQREKI 839
781 REQMQRYNQRMIEQLKVRQQQEKKARLPKIQRSEGKTRMAMYKKSLHINGGGSAEQREKI 840

*****
840 KQFSQQEKKRQKAERLQQQKKHEHQMRDMVAQCESNMSELQQQLQNEKCYLLVEHETQKCLK 899
841 KQFSQQEKKRQKSERLQQQKKHENQMRDMLAQCESNMSELQQQLQNEKCHLLVEHETQKCLK 900

*****
900 ALDESHNQSLKE 911
901 ALDESHNQNLKE 912

```

Fig. 6C

PAK1_h	MSNGLDIQDKPPAPPMRNTSTMIGAGSKDAGTL	NHGS	KPLPP	NPEEK	KKKDRFYRSIL	59
PAK65_h	MEETQQKSHLELLSA	----	NHSL	KPLPS	VPEEK	KPRHKIIISIFS
PAK3_m	-MSDSLNDNEEKPPAPPLR	----	MNSN	NRDSSAL	NHSS	KPLPMAPEEK
						NKKARLSIFPG
						54
PAK1_h	PGDK	TNKKKEKERPEIS	LP	PSDFEHT	IHVGFDA	VTGEFT
						GMPEQ
						WARLLQTSNIT
						KS
						115
PAK65_h	GTEK	GSKKKEKERPEIS	PP	PSDFEHT	IHVGFDT	VTGEFT
						GMPEQ
						WARLLQTSNIT
						KL
						96
PAK3_m	GGDK	TNKKKEKERPEIS	LP	PSDFEHT	IHVGFDA	VTGEFT
						GIPEQ
						WARLLQTSNIT
						KL
						110
PAK4_h	----	MFR	KKKKRPEISA	PQNF	QHRVHTS	FDPK
						EGKFV
						GLPPQ
						WQNI
						LDIT
						LRRPK
						PVVDP
						56
PAK1_h	----	----	----	----	----	----
						115
PAK65_h	----	----	----	----	----	----
						96
PAK3_m	----	----	----	----	----	----
						110
PAK4_h	SRITRV	QLQPMKTVVRGS	AMPVDGYISGL	LLNDIQKLS	VISSNT	LRGRSPTS
						RRRAQSLGL
						116
PAK1_h	----	----	----	----	----	----
						115
PAK65_h	----	----	----	----	----	----
						96
PAK3_m	----	----	----	----	----	----
						110
PAK4_h	LGDEH	WATDPDMYLQSPQ	SERTDPHGLY	LSCN	GGTPAGHK	QMPWPEPQ
						SPRVLP
						PNGLAAK
						176
PAK1_h	----	----	----	----	----	----
						EQKKNPQ
						AVLDV
						127
PAK65_h	----	----	----	----	----	----
						EQKKNPQ
						AVLDV
						108
PAK3_m	----	----	----	----	----	----
						EQKKNPQ
						AVLDV
						122
PAK4_h	AQSLG	PAEFQGASQRCLQLG	ACLQSSPPGAS	PPPTGTNR	HGMKA	AKHGS
						SE
						EARPQ
						SCLVGS
						236

Fig. 7A

PAK1_h	L	E	F	Y	N	S	K	K	T	S	N	S	Q	K	Y	M	S	F	T	--	D	K	S	A	E	D	Y	N	S	S	N	A	L	N	V	K	A	V	S	E	T	P	A	V	P	P	V	S	E	D	E	D	D	D	D	D	A	T	185																	
PAK65_h	L	K	F	Y	D	S	--	N	T	V	K	Q	K	Y	L	S	F	T	--	P	P	E	K	D	G	F	P	S	G	T	P	A	L	N	A	K	G	T	E	A	P	A	V	T	--	E	E	E	D	D	D	E	E	T	160																					
PAK3_m	L	K	F	Y	D	S	K	E	T	V	N	N	Q	K	Y	M	S	F	T	S	G	D	K	S	A	H	G	Y	I	A	A	H	Q	S	N	T	K	T	G	S	E	P	L	A	P	P	V	S	E	E	E	E	E	E	E	E	182																			
PAK4_h	A	T	G	R	P	G	G	E	G	S	P	S	P	K	T	R	E	S	S	L	K	R	R	L	F	R	S	M	F	L	S	T	A	A	T	A	P	P	S	S	S	K	P	G	P	P	P	Q	S	K	P	N	S	S	F	R	P	P	Q	K	296															
PAK5_h	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	A	S	G	A	K	L	A	A	G	R	P	F	N	T	14											
PAK1_h	--	--	--	--	P	P	P	V	I	A	P	R	P	E	H	T	K	S	V	Y	T	R	S	V	I	E	P	L	P	V	T	P	T	R	D	V	A	T	S	P	I	S	P	T	E	N	N	T	T	P	P	D	A	L	T	L	N	T	E	K	241															
PAK65_h	--	--	--	--	A	P	P	V	I	A	P	R	P	D	H	T	K	S	I	Y	T	R	S	V	I	D	P	V	P	A	P	V	G	D	S	H	V	D	G	A	A	K	S	L	--	--	--	--	--	--	--	--	--	--	--	--	--	D	K	202																
PAK3_m	D	D	N	E	P	P	P	V	I	A	P	R	P	E	H	T	K	S	I	Y	T	R	S	V	V	E	S	I	A	S	P	A	A	P	N	K	E	D	I	P	P	S	A	E	N	A	N	S	T	T	L	Y	R	--	--	N	T	D	R	239																
PAK4_h	D	N	P	P	S	L	V	A	K	A	Q	S	L	P	S	D	Q	P	V	G	T	F	S	P	L	T	T	S	D	T	S	S	P	Q	K	S	L	R	T	A	P	A	T	G	Q	L	P	G	R	S	S	P	A	--	--	G	S	P	R	353																
PAK5_h	Y	P	R	A	D	T	D	H	P	S	R	G	A	Q	G	E	P	H	D	V	A	P	N	G	P	S	A	G	G	L	A	I	P	Q	S	S	S	S	S	S	R	P	P	T	R	A	R	G	A	P	S	P	G	V	L	G	P	H	A	S	74															
PAK1_h	Q	K	K	K	P	K	M	S	D	E	E	I	L	E	K	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	L	R	S	I	V	S	V	G	D	P	K	K	K	Y	T	R	F	E	K	I	276			
PAK65_h	Q	K	K	K	T	K	M	T	D	E	E	I	H	E	K	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	L	R	T	I	V	S	I	G	D	P	K	K	K	Y	T	R	Y	E	K	I	237	
PAK3_m	Q	R	K	K	S	K	M	T	D	E	E	I	L	E	K	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	L	R	S	I	V	S	V	G	D	P	K	K	K	Y	T	R	L	E	K	I	274
PAK4_h	T	W	H	A	Q	I	S	T	S	N	L	Y	L	P	Q	D	P	T	V	A	K	G	A	L	A	G	E	D	T	G	V	V	T	H	E	Q	F	K	A	A	L	R	M	V	V	D	Q	G	D	P	R	L	L	L	D	S	Y	V	K	I	413															
PAK5_h	E	P	Q	L	A	P	P	A	C	T	P	A	A	V	P	G	P	P	R	S	P	Q	R	E	P	Q	R	V	S	H	E	Q	F	R	A	A	L	Q	L	V	V	D	P	G	D	P	R	S	Y	L	D	N	F	I	K	I	134																			
PAK1_h	G	Q	G	A	S	G	T	V	Y	T	A	M	D	V	A	T	G	Q	E	V	A	I	K	Q	M	N	L	Q	Q	P	K	K	E	L	I	I	N	E	I	L	V	M	R	E	N	K	N	P	N	I	V	N	Y	L	D	S	Y	L	V	336																
PAK65_h	G	Q	G	A	S	G	T	V	F	T	A	T	D	V	A	L	G	Q	E	V	A	I	K	Q	I	N	L	Q	Q	P	K	K	E	L	I	I	N	E	I	L	V	M	K	E	L	K	N	P	N	I	V	N	F	L	D	S	Y	L	V	297																
PAK3_m	G	Q	G	A	S	G	T	V	Y	T	A	L	D	I	A	T	G	Q	E	V	A	I	K	Q	M	N	L	Q	Q	P	K	K	E	L	I	I	N	E	I	L	V	M	R	E	N	K	N	P	N	I	V	N	Y	L	D	S	Y	L	V	334																
PAK4_h	G	E	G	S	T	G	I	V	C	L	A	R	E	K	H	S	G	R	Q	V	A	V	K	M	M	D	L	R	K	Q	Q	R	R	E	L	L	F	N	E	V	I	M	R	D	Y	Q	H	F	N	V	V	E	M	Y	K	S	Y	L	V	473																
PAK5_h	G	E	G	S	T	G	I	V	C	I	A	T	V	R	S	S	G	K	L	V	A	V	K	M	D	L	R	K	Q	Q	R	R	E	L	L	F	N	E	V	I	M	R	D	Y	Q	H	E	N	V	V	E	M	Y	N	S	Y	L	V	194																	

Fig. 7B

PAK1_h	GDELWVVM EYLAGGSLTDVVVTETCTMDEGQIAAVCRECLQAL	ESLH	SNQVIHRDIKSDN	IL	396
PAK65_h	GDEL[FV]VM EYLAG[R]SLTDVVVTETCTMDEAQIAAVCRECLQAL	EFFL	HANQVIHRDIKSDN	VL	357
PAK3_m	GDELWVVM EYLAGGSLTDVVVTETCTMDEGQIAAVCRECLQAL	DFLH	SNQVIHRDIKSDN	IL	394
PAK4_h	G[E]ELWV[L]M[E]F[L]QGGALTDIIVSQVRLN[E]EQIA[T]VCEAVLQAL	AYLH	AQQGVIIHRDIKSD	SIL	533
PAK5_h	GDELWVVM EYFLEGGALTDIIVT[H]TR[M]NEEQIAAVCLAVLQAL	SVLH	AQQGVIIHRDIKSD	SIL	254
PAK1_h	LGM DGSVKLTDFGFCAQITPEQSKRSTMVGTPTYWMAPEVVTRKAYGPKVDIWSL	GIMA	IE	456	
PAK65_h	LGM[E]GSVKLTDFGFCAQITPEQSKRSTMVGTPTYWMAPEVVTRKAYGPKVDIWSL	GIMA	IE	417	
PAK3_m	LGM DGSVKLTDFGFCAQITPEQSKRSTMVGTPTYWMAPEVVTRKAYGPKVDIWSL	GIMA	IE	454	
PAK4_h	L[T]LDGRV[K]L[S]DFGFCAQISKDVPKR[K]SLVGTPTYWMAPEV[IS]RSLYATEV	DIWSL	GIMVIE	593	
PAK5_h	L[TH]DGRV[K]L[S]DFGFCAQVSK[E]VPRR[K]SLVGTPTYWMAPELISRLPYGP	IE	314		
PAK1_h	M[IE]GEPYPYL NENPLRALYLIATNGTPELQNPEKLSAIFRDFLNRCLEMDV	IE	KRGSAKELL	516	
PAK65_h	MVEGEPYPYL NENPLRALYLIATNGTPELQNPEKLSPIIFRDFLNRCLEMDV	IE	KRGSAKELL	477	
PAK3_m	MVEGEPYPYL NENPLRALYLIATNGTPELQNPERLSAV[FH]DFLNRCL	MDVDR	RGSAKELL	514	
PAK4_h	MVDGEPYPYFSDSPVQAMKRLRDSPPK[L]KNSHKVSPVLRD[F]L	ERM	LVRDPQERATTAQELL	653	
PAK5_h	MVDGEPYPYFNEPPL[K]A[M]KMI[R]D[N]LPRL[K]N[L]HKVSPSLKGF	LDR	LVRDPAQRATAELL	374	
PAK1_h	Q[H]Q[FL]K[I]AKPLSSLTPLIIAAAKEA[T]KNNH			545	
PAK65_h	QHPFLK[L]AKPLSSLTPLIIMAAAKEAMKSNR			506	
PAK3_m	QHPFLK[L]AKPLSSLTPLIIIAAKEA[I]KNSR			544	
PAK4_h	DHPFL[Q]TGLPEC[L]VPLI[Q]LYRKQTSTC			681	
PAK5_h	KHPFLAKA[G]PPA[S]IVPLMRQNRTR			398	

Fig. 7C

SEQ ID NO: 5 STLK2 human Nterm=1-21 kin=22-274
Cterm=275-416

MAHSPVAVQVPGMQNNIADPEELFTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEA
EDEIEDIQQEITVLSQCDSSYVTKEYYSYLKGSKLWIIMEYLGSGSALDLLRAGPFDEFQ
IATMLKEILKGLDYLHSEKKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFV
GTPFWMAPEVIQQSAYDSKADIWSLGITAIELAKGEPPNSDMHMPMRVLFLIPKNNPPTLV
GDFTKSFKEFIDACLNKDPSFRPTAKELLKHKFIVKNSKTSYLTTELIDRFKRWKAEGHS
DDES DSEGS DSESTSRENTHPEWSFTTVRKKPDPKKVQNGAEQDLVQTLSCLSMIITPA
FAELKQQDENNASRNQAIEELEKSI AVAEAAACPGITDKMVKKLIEKFQKCSADESP

SEQ ID NO: 6 STLK3 human Nterm=1-31 kin=32-308 Cterm=309-489
(insert=327-352) tail=490-516

TAAPAPAAPAAPAPAPAPAPAAQAVGWPICRDAYELQEVIGSGATAVVQAALCKPRQERV
AIKRINLEKCQTSMDLLKEIQAMSQC SHPNVVTTYTSFVVKDELWLVMKLLSGGSMLDI
IKYIVNRGEHKNVLEEAIATILKEVLEGLDYLRNGQIHRDLKAGNILLGEDGSVQIA
DFGVSAFLATGGDVTRNKVRKTFVGTPCWMAPEVMEQVRGYDFKADMWSFGITAIELATG
AAPYHKYPPMKVLM LTLQNDPPTLETGVEDKEMMKKYGKSFRKLLSLCLQKDPSKRPTAA
ELLKCKFFQKAKNREY LIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWEWSDDDEM
DEKSEEGKAAFSQEKSRRVKEENPEIAVSASTIPEQIQSLSVHDSQGPPNANEDYREASS
CAVNLVLRRLRNSRKELNDIRFEFTPGRDTADGVSQELFSAGLVDGHDVVIVAANLQKIVD
DPKALKTLTFKLASGCDGSEIPDEVKLIGFAQLSVS

SEQ ID NO: 7 STLK4 human Nterm=absent, kin=1-178, Ctail=179-414,
insert1=198-222, insert2=253-293

KSGVLDXSTIATILREVLEGLEYLHKXGQIHRDVKAGNILXGEDGSVQIADFGVSAFLAT
GGDITRNKVRKTFVGTPCWMAPEVMEQVRGYDFKADIWSFGITAIELATGAAPYHKYPPM
KVLMLTLQNDPPSLETGVQDKEMLKKYGKSFRKMISLCLQKDPEKRPTAAELLRHKFFQK
AKNKEFLQEKT LQ RAPTISERAKKVRVP GSSGRLHKTEDGGWEWSDDDEFDEESEEGKAA
ISQLRSPRVKESISNSELFPTTDPVGTL LQVPEQISAHLPQPAQGIATQPTQVSLPPTAE
PAKTAQALSSGSGSQETKIPISLVRLRNSKKELNDIRFEFTPGRDTAEGVSQELISAGL
VDGRDLVIVAANLQKIVEEPQSNRSVTFKLASGVEGSDIPDDGKLIGFAQLSIS

SEQ ID NO: 8 STLK5 human Nterm=absent, kin=1-222(lacks N-term),
Ctail=224-274

LICTHFMDGMNELAIAYILQGV LKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRSN
LSMISHGQRQRVVHDFPKYSVKVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHV
PFKDMPATQMLLEKLN GTVPCLLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNG
DSPSHPHYHRTFSPHFHHFVEQCLQRNP DARPSASTLLNHSFFKQIKRRASEALPELLRPV

TPITNFEGSQSQDHSGIFGLVTNLEELEVDDEWF

SEQ ID NO: 13 ZC1 human 1/5/98 Nterm=1-22 kin=23-289

coiled-coil=290-526 pro=527-640 B=641-896 Rab/Rac-BD=897-1239

MANDSPAKSLVDIDLSSLRDPAGIFELVEVVGNGTYGQVYKGRHVKTGQLAAIKVMDVTE
DEEEEIKLEINMLKKYSHHRNIATYYGAFIKKSPPGHDDQLWLVMFEFCGAGSITDLVKNT
KGNTLKEDWIAYISREILRGLAHLHIHHVIHRDIKGQNVLLTENAEVKLVDFGVSAQLDR
TVGRRNTFIGTPYWMAPEVIACDENPDATYDYRSDLWSCGITAIEMAEGAPPLCDMHPMR
ALFLIPRNPPRLKSKKWSKKFFSFIEGCLVKNYMQRPSTEQLLKHPFIRDQPNERQVRI
QLKDHIDRTRKKRGEKDETEYEYSGSEEEEEVPEQEGEPSSIVNVPGESTLRRDFLRQLQ
QENKERSEALRRQQLLEQQQLREQEEYKRQLLAERQKRIEQQKEQRRRLEEQQRREREAR
RQQEREQRRREQEEKRRLEELERRRKEEEEERRRAEEEKRRVEREQEYIRRQLEEEQRHLE
VLQQQLLEQAMLLRCRWREMEHRQAERLQRQLQQEQAYLLSLQHDHRRPHPQHSQQPP
PPQQERSKPSFHAPEPKAHYEPADRAREVEDRFRKTNHSSPEAQSKQTGRVLEPPVPSRS
ESFSNGNSESVHPALQRPAEPQVPVRTTSRSPVLSRRDSPLOQSGGQQNSQAGQRNSTSIE
PRLLWERVEKLVPRPGSGSSSGSSNSGSQPGSHPGSQSGSGERFRVRSSSKSEGSPSQRL
ENAVKKPEDKKEVFRPLKPADLTALAKELRAVEDVRPPHKVTDYSSSSEESGTTDEEDDD
VEQEGADESTSGPEDTRAASSLNLSNGETESVKTMIVHDDVESEPAMTPSKEGTLIVRRT
QSASSTLQKHKSSSSFTPFIDPRLLQISPSSGTTVTSVVGFSCDGMRPEAIRQDPTRKGS
VVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGVNLLVGTESGLMLLDRSGQGKVYP
LINRRRFQQMDVLEGLNVLVLTISGKKDKLRVYYLSWLRNKLHNDPEVEKKQGWTTVGDL
EGCVHYKVVKYERIKFLVIALKSSVEVYAWAPKPYHKFMAFKSFGELVHKPLLVDLTVEE
GQRLKVIYIGSCAGFHAVDVDGSGSVYDIYLPHTHIQCSIKPHAIILPNTDGMELLVCYEDE
GVYVNTYGRITKDVLVQWGEMPTSVAYIRSNQTMGWGEKAIEIRSVETGHLDGVFMHKRA
QRLKFLCERNDKVFFASVRSGGSSQVYFMTLGRTSLLSW

SEQ ID NO: 14 ZC2 human Nterm=missing kin=1-255 coiled-coil=256-442
pro=443-626 B=627-954 Rab/RacBD=955-1297

AFGEVYEGRHVKTGQLAAIKVMDVTGDEEEEIKQEIINMLKKYSHHRNIATYYGAFIKKNP
PGMDDQLWLVMFEFCGAGSVTDLIKNTKGNTLKEEWIAYICREILRGLSHLHQHKVIHRDI
KGQNVLLTENAEVKLVDFGVSAQLDRTVGRRNTFIGTPYWMAPEVIACDENPDATYDFKS
DLWSLGITAIEMAEGAPPLCDMHPMRALFLIPRNPAAPRLKSKKWSKKFQSFIESCLVKNH
SQRPATEQLMKHPFIRDQPNERQVRIQLKDHIDRTRKKRGEKDETEYEYSGSEEEEEEND
SGEPSSILNLPRESTLRRDFLRQLANKERSEALRRQQLLEQQQRENEEHKRQLLAERQKR
IEEQKEQRRRLEEQQRRREKELRKQQEREQRRHYEEQMRREEERRRAEHEQEYKRKQLEEQ
RQAERLQRQLKQERDYLVSQHQHQEQRPVEKKPLYHYKEGMSPSEKPAWAKEVEEERSRL
NRQSSPAMPHKVANRISDPNLPRESSESFSISGVQPARTPPMLRPVDPQIPHLVAVKSQGP
ALTASQSVHEQPTKGLSGFQEALNVTSHRVEMPRQNSDPTSENPLPTRIEKFDRSSWLR

Fig. 8B

27/76

QEEDIPPKVPQRTTSSISPALARKNSPGNGSALGPRLGSQPIRASNPDLRRTEPILESPLQ
RTSSGSSSSSSSTPSSQPSQGGSQPGSQAGSSERTRVRANSKSEGSVLPHEPAKVKEE
SRDITRPSRPASYKKAIDEDLTALAKELRELRIEETNRPMKKVTDYSSSSSEESSESEEE
EDGESETHDGTVAVSDIPRLIPTGAPGSNEQYNVGMVGTHGLETSHADSFSGSISREGTL
MIRETSGEKKRSGHSDSNGFAGHINLPDLVQQSHSPAGTPT EGLGRVSTHSQEMDSGTEY
GMGSSTKASFTPFVDPRVYQTSPTDEDEDEEESAAALFTGELLRQEQA K LNEARKISVV
NVNPTNIRPHSDTPEIRKYKKRFNSEILCAALWGVNLLVGTENGLMLLDRSGQGKVYNLI
NRRRFQQMDVLEGLNVLVTISGKKNKLRVYYLSWLRNRILHNDPEVEKKQGWITVGDLEG
CIHYKVVKYERIKFLVIALKNAVEIYAWAPKPYHKFMAFKSFADLQHKPLLVDLTVEEGQ
RLKVIFGSHTGFHVIDVDSGNSYDIYTPSHIQGNITPHAIVILPKTDGMEMLVCYEDEGV
YVNTYGRITKDVVLQWGEMPTSVAYIHSNQIMGWGEKAIEIRSVETGHL DGVFMHKRAQR
LKFLCERN DKVFFASVRS GGSSQVFFMTLNRNSMMNW

SEQ ID NO: 15 ZC3 human kin=1-255 coiled-coil=256-476 pro=477-680
B=681-983 Rab/RacBD =984-1326

AFGEVYEGRHVKTGQLAAIKVMDVTEDEEEEIKQEINMLKKYSHHRNIATYYGAFIKKSP
PGNDDQLWLVMFCGAGSVTDLVKNTKGNALKEDCIAYICREILRGLAHLHAHKVIHRDI
KGQNVLLTENA EVKLVD FGVSAQLDRTVGRRNTFIGTPYWM APEVIACDENPDATYDYRS
DIWSLGITAIEMAEGAPPLCDMHPMRALFLIPRNPPRLKSKKWSKKFIDFIDTCLIKTY
LSRPPT EQLLKFPFIRDQPTERQVRIQLKDHIDRSRKKRGEKEETEY EYSGSEEEDDSHG
EEGEPSSIMNVPGESTLRREFLRLQQENKSNSEALKQQQQQLQQQQQRDPEAHIKHLLHQR
QRRIEEQKEERRRVEEQRRREREQRKLQEKEQRRLED MQALRREEERRQAEREQEYIRH
RLEEEQRQLEILQQQLLQEQA L LLEYKRKQLEEQRQSERLQRQLQ QEHAYLKS LQQQQQ
QQLQKQQQQQLLPGDRKPLYHYGRGMNPADKPAWAREVEERTRMNKQQNSPLAKSKPGST
GPEPPIPQASPGPPGPLSQTTPMQRVPEQEGPHKSLVAHRVPLKPYAAPVPRSQSLQDQ
PTRNLAAFPASHDPDPAIPAPTATPSARGAVIRQNSDPTSEGPGPSNPPAWVRPDNEAP
PKVPQRTSS IATALNTSGAGGSRPAQAVRARPRSNSAWQIYLQRR AERGTPKPPGPPAQP
PGPPNASSNPDLRRSDPGWERSDSVLPASHGHL PQAGSLERNRVGVSSKPDSSPVLSPGN
KAKPDDHRSRPGRPADFVLLKERTLDEAPRPPKKAMDYSSSSSEEVESSEDEEEGEGGPA
EGSRDTPGGRDGD TDSVSTMVVDVEEITGTQPPYGGGT MVVQRTPEEERNLLHADSNGY
TNLPDVVQPSHSPTENSKGQSPPSKDGSGDYQSRGLVKAPGKSSFTMFVDLGIYQPGGSG
DSIPITALVGGEGTRLDQLQYDVRKGSVVNVNPTNTRAHSETPEIRKYKKRFNSEILCAA
LWGVNLLVGTENGLMLLDRSGQGKVYGLIGRRRFQQMDVLEGLNLLITISGKR NKLRVYY
LSWLRNKILHNDPEVEKKQGWTTVGDMEGCGHYRVVKYERIKFLVIALKSSVEVYAWAPK
PYHKFMAFKSFADLPHRPLLVDLTVEEGQRLKVIYGSSAGFHAVD VDSGNSYDIYIPVHI
QSQITPHAIIFLPNTDGMEMLLCYEDEGVYVNTYGR I IKDVVLQWGEMPTSVAYICSNQI
MGWGEKAIEIRSVETGHL DGVFMHKRAQR LKFLCERN DKVFFASVRS GGSSQVYFMTLNR
NRIMNW

Fig. 8C
28/76

SEQ ID NO: 16 ZC4 human Nterm kin coiled-coil pro B=missing
Rab/RacBD=1-349

NVNPLYVSPACKKPLIHMYEKEFTSEICCGSLWGVNLLLGTRSNLYLMDRSGKADITKLI
RRRPFRQIQVLEPLNLLITISGHKNRLRVYHLTWLRNKILNNDPESKRRQEEMLKTEEAC
KAIDKLTGCEHFSVLQHEETTYIAIALKSSIHLYAWAPKSFDESTAIKVFPPTLDHKPVTV
DLAIGSEKRLKIFFSSADGYHLIDAESEVMSDVTLPKNPLEIIIPQNIIILPDCLGIGMM
LTFNAEALSVEANEQLFKKILEMWKDIPSSIAFECTQRTTGWGQKAIEVRSLQSRVLESE
LKRRSIKKLRFLCTRGDKLFFTSTLRNHHSRVYFMTLGKLEELQSNDY

SEQ ID NO: 18 KHS2 human Nterm=1-13 kin=14-273 A=274-346
Pro=347-534 RabBD =535-894

MNPGFDLSRRNPQEDFELIQRIGSGTYGDVYKARNVNTGELAAIKVIKLEPGEDFAVVQQ
EIIMMKDCKHPNIVAYFGSYLRRDKLWICMEFCGGGSLQDIYHVTGPLSELQIAYVSRET
LQGLYYLHSGKGMHRDIKGANILLTDNGHVKLADFGVSAQITATIAKRKSFITPYWMA
EVAVERKGGYNQLCDLWAVGITAIELAEQPPMFDLHPMRALFLMTKSNFQPPKLKDKM
KWSNSFHHFVKMALTKNPKKRPTAEKLLQHPFVTQHLTRSLAIELLDKVNPNPDHSTYHDF
DDDDPEPLVAVPHRIHSTSRNVREEKTRSEITFGQVKFDPPLRKETEPHHELPDSDGFLD
SSEIYYTARSNLDLQLEYGQGHQGGYFLGANKSLLKSVEEELHQRGHVAHLEDDEGDD
ESKHSTLKAKIPPLPPPKPSIFIPQEMHSTEDENQGTIKRCMSGSPAKPSQVPPRPPP
PRLPPHKPVALGNGMSSFQLNGERDGSQCQQQNEHRGTNLSRKEKKDVPKPI SNGLPPTP
KVHMGACFSKVFNGCPLKIHCASSWINPDTRDQYLIFGAEEGIYTLNLNELHETSMEQLF
PRRCTWLYVMNNCLLSISGKASQLYSHNLPGLFDYARQMQLPVAIPAHKLPDRILPRKF
SVSAKIPETKWCQKCCVVRNPYTGHKYL CGALQTSIVLLEWVEPMQKFMLIKHIDFPIPC
PLRMFEMLVVPEQEYPLVCVGVSRGRDFNQVVRFETVNPNSTSSWFTESDTPQTNVTHVT
QLERDTILVCLDCCIKIVNLQGRKSSRKLSSSELTDFDQIESIVCLQDSVLAFWKHGMQG
RSFRSNEVTQEISDSTRIFRLLGSDRVVLESRPTDNPTANSNLYILAGHENSY

SEQ ID NO: 22 SULU1 human N=1-21 kin=22-277 A=278-427
coiled-coil1=428-637 B=638-751 coiled-coil2=752-898

MRKGVLDKDEIDDLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTNEVVAIKKMSYSGK
QTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMYCLGSASDLLLVHKKPLQ
EVEIAAITHGALHGLAYLHSHALHRDIKAGNILLTEPGQVKLADFGSASMASPANSFVG
TPYWMAPEVILAMDEGQYDGKVDIWSLGITCIELAERKPPLFNMNAMSALYHIAQNDSPT
LQSNEWTDSFRRFVDYCLQKIPQERPTSAELLRHDFVRRDRPLRVLIDLIQRTKDAVREL
DNLQYRKMKKILFQETRNGPLNESQEDEEDSEHGTSLNREMSLGSNHSIPSMSVSTGSQ
SSSVNSMQEVMDESSSELVMMHDESTINSSSSSVVHKKDHVFTRDEAGHGDPPEPRPTQ
SVQSQUALHYRNRERFATIKSASLVTRQIHEHEQENELREQMSGYKRMRRQHQQQLIALEN
KLKAEMDEHRLKLQKEVETHANNSSIELEKLAKKQVAIIEKEAKVAAADEKKFQQQILAQ

QKKDLTTFLESQKKQYKICKEKIKEEMNEDHSTPKKEKQERISKHKENLQHTQAEAAAHL
LTQQRLYYDKNCRFFKRKIMIKRHEVEQQNIREELNKKRTQKEMEHAMLIRHDESTRELE
YRQLHTLQKLRLMDLIRLQHQTelenQLEYNKRERELHRKHVMGLRQQPKNLKAMEMQIK
KQFQDTCKVQTKQYKALKNHQLEVTPKNEHKTILKTLKDEQTRKLAILAEQYEQSINEMM
ASQALRLDEAQEAECQALRLQLQQEMELLNAYQSKIKMQTEAQHERELQKLEQRVSLRRA
HLEQKIEEEELAAALQKERSERIKNLLERQEREIETFDMESLRMGFGNLVTLDFPKEDYR

SEQ ID NO: 23 SULU3 human Nterm=missing kin partial=1-66 A=67-215
coiled-coil1=216-425 B=426-539 coiled-coil2=540-786 Ctail=687-786
IELAERKPPLFNMNAMSALYHIAQNESPTLQSNEWSDYFRNFVDSCLQKIPQDRPTSEEL
LKHIFVLRRERPETVLIDLIQRTKDAVRELDNLQYRKMKLLFQEAHNGPAVEAQEEEEEQ
DHGVGRTGTVNSVGSNQSI PSMSISASSQSSSVNSLPDVSDDKSELDMMEGDHTVMSNSS
VIHLKPEEENYREEGDPRTASDPQSPQVSRHKSHYRNREHFATIRTSASLVTRQMQEHE
QDSELREQMSGYKRMRRQHQQQLMTLENKLKAEMDEHRLRLDKDLETQRNNFAAEMEKL
KKHQAAMEKEAKVMSNEEKKFQQHIQAQQKKELNSFLESQKREYKLRKEQLKEELNENQS
TPKKEKQEWLSKQKENIQHFQAEAAEANLLRRQRQYLELECRRFKRRMLLGRHNLEQDLVR
EELNKRQTQKDLEHAMLLRQHESMQELEFRHLNTIQKMRCELIRLQHQTENQLEYNKR
RERELRRKHVMEVRQQPKSLKSKELQIKKQFQDTCKIQTRQYKALRNHLLLETPKSEHKA
VLKRLKEEQTRKLAILAEQYDHSINEMLSTQALRLDEAQEAECQVLKMQQLQEELELLNAY
QSKIKMQAEAQHDRELRELEQRVSLRRALLEQKIEEEMLALQNERTERIRSLERQAREI
EAFDSESMRLGFSNMVLSNLSPEAFSHSYPGASGWSHNPTGGPGPHWGHPMGGPPQAWGH
PMQGGPQPWGHPSGPMQGVPRGSSMGVRNSPQALRRRTASGGRTEQGMSRSTSVTSQISNG
SHMSYT

SEQ ID NO: 24 SULU3 murine Nterm=1-25 kin=26-273 A=274-422
cc1=423-632 B=633-748 cc2=missing
MPSTNRAGSLKDPEIAELFFKEDPEKLFTDLREIGHGSFGAVYFARDVRTNEVVAIKKMS
YSGKQSTEKWQDIIKEVKFLQRIKHPNSIEYKGCYLREHTAWLVM EYCLGSASDLLLEVHK
KPLQEEVEIAAITHGALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMASPAN
SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN
ESPTLQSNMNDSC LQKIPQDRPTSEELLKHMFLRRERPETVLIDLIQRTKDAVRELDNLQ
YRKMKLLFQEAHNGPAVEAQEEEEEQDHGVGRTGTVNSVGSNQSI PSMSISASSQSSSV
NSLPDASDDKSELDMMEGDHTVMSNSSVIHLKPEEENYQEEGDPRTASDPQSPQVSRH
KSHYRNREHFATIRTSASLVTRQMQEHEQDSELREQMSGYKRMRRQHQQQLMTLENKLKAE
MDEHRLRLDKDLETQRNNFAAEMEKLKKHQAAMEKEAKVMA NEEKKFQQHIQAQQKKEL
NSFLESQKREYKLRKEQLKEELNENQSTPKKEKQEWLSKQKENIQHFQAEAAEANLLRRQR
QYLELECRRFKRRMLLGRHNLEQDLVREELNKRQTQKDLEHAMLLRQHESMQELEFRHLN
TIQKMRCELIRLQHQTENQLEYNKRERELRRKHVMEVRQQPKSLKSKELQIKKQFQD

Fig. 8E
30/76

TCKIQTRQYKALRNHLLLETPKNEHKAI

SEQ ID NO: 26 GEK2 human N=1-33 kin=34-294 A=295-337 B=338-472 215
coiled-coil1=473-724 215 coiled-coil2=725-912
MAFANFRRLRLSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVYKAKNKETGA
LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYHDGKLWIMIEFCPPGGAVDA
IMLELDRGLTEPQIQVVCQRQMLEALNFLHSKRRIHRDLKAGNVLMTLEGDIRLADFGVSA
KNLKTLLQKRDSFIGTPYWMAPEVVMCETMKDTPYDYKADIWSLGITLIEMAQIEPPHHEL
NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLEHPFVSSITSN
KALRELVAEAKAEVMEEIEDGRDEGEEEDAVIDAASSTLENHTQNSSEVSPPSLNADKPLEE
SPSTPLAPSQSQDSVNEPCSQPSGDRSLQTTSPPVVAPGNENGLAVPVPLRKS RVPVSM DA
RIQVAQEKQVAEQGGDLSPAANRSQKASQSRPNSSALETLGGEKLANGSLEPPAQAAPGP
SKRSDSCSSLCTSESMDYGTNLSTDLSLNKEMGSLSIKDPKLYKKTLLKRTKRFVVDGVEV
SITTSKIISEDEKKDEEMRFLRRQELRELRLLLQKEEHRNQTQLSNKHELQLEQMHRFEQ
EINAKKKFFDTELENLERQQKQQVEKMEQDHAVRRREEARRIRLEQDRDYTRFQEQLKLM
KKEVKNEVEKLPRQQRKESMKQKMEEHTQKKQLLDRDFVAKQKEDLELAMKRLTTDNRR
ICDKERECLMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHELLRKHEKE
REQMQRYNQRMIEQLKVRQQQEKARLPKIQRSEGKTRMAMYKKSLHINGGGSAAEQREKI
KQFSQQEEKRQKSERLQQQQKHENQMRDMLAQCESNMSELQQQLQNEKCHLLVEHETQKLK
ALDESHNQN LKE

SEQ ID NO: 29 PAK4 human Rac=1-51 A=52-224 Nterm=225-393
kin=394-658 Ctail=659-681 residues 13-23
(SAPQNFQHRVH)= Cdc42 /Rac-binding motif
MFRKKKKKRPEISAPQNFQHRVHTSFDPKEGKFVGLPPQWQNILDTLRRPKPVVDPSRIT
RVQLQPMKTVVRGSAMPVDGYISGLLNDIQKLSVISSNTLRGRSPTSRRRAQSLGLLGDE
HWATDPDMYLQSPQSERTDPHGLYLSCNGGTPAGHKQMPWPEPQSPRVLPNGLAAKAQSL
GPAEFQGASQRCLQLGACLQSSPPGASPTGTNRHGMKAAKHGSEEARPQSCLVGSATGR
PGGEGSPSPKTRESSLKRRFLFRSMFLSTAATAPPSSSKPGPPPQSKPNSSFRPPQKDNPP
SLVAKAQSLPSDQPVGTFSPLTTSSTSSPQKSLRTAPATGQLPGRSSPAGSPRTWHAQIS
TSNLYLPQDPTVAKGALAGEDTGVTHEQFKAALRMVVDQGDPRLLLLDSYVKIGEGSTGI
VCLAREKHSGRQVAVKMDLRKQQRRELLFNEVVIMRDYQHFNVEMYKSYLVGEELWVL
MEFLQGGALTDIVSQVRLNEEQIATVCEAVLQALAYLHAQGVHRDIKSDSILLTLDGRV
KLSDFGFCAQISKDVPKRKSLVGTPYWMAPEVISRSLYATEVDIWSLGIMVIEMVDGEP
YFSDSPVQAMKRLRDSPPPKLKNSHKVSPVLRDFLERMLVRDPQERATAQELL DHPFL LQ
TGLPECLVPLIQLYRKQTSTC

Fig. 8F
31/76

SEQ ID NO: 30 PAK5 human Rac A=missing Nterm partial=1-114
kin=115-379 Ctail=380-398

ASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAPNGPSAGGLAIPQSSSSSSSRPPTRA
RGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQREPQRVSHEQFRAALQLVVD
PGDPRSYLDFIKIGEGSTGIVCIATVRSSGKLVAVKKMDLRKQQRRELLFNEVVIMRDY
QHENVVEMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA
QGVHRDIKSDSILLTHDGRVKLSDFGFCAQVSKEVPRRKSLVGTPYWMAPELISRLPYG
PEVDIWSLGIMVIEMVDGEPPYFNEPPLKAMKMIRDNLPPRLKNLHKVSPSLKGFLDRLL
VRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR

Fig. 8G

SEQ ID NO: 1 STLK2 HUMAN

TAACAGCCCCACCTCCTAGCCCCGGGCTACGCGCCGCCAGCCCAGTAACCCCACTTTTGTG
TGTCCTCCCAGGCCCCGATCGAAAAGCCTGGGAGGGCCGCCGAAC TACCCCGGAGGGAG
GAGCCAGTCCGAACCCAAGGCGCCACCGCCGCAGAAGCGGAGCGAGGCAGCATTTCGCCTC
CATGGCCCCACTCGCCGGTGGCTGTCCAAGTGCCTGGGATGCAGAATAACATAGCTGATCC
AGAAGAACTGTTCACAAAAATTAGAGCGCATTGGGAAAAGGCTCATTTGGGGAAAGTTTTCAA
AGGAATTGATAACCGTACCCAGCAAGTCGTTGCTATTTAAAATCATAGACCTTGAGGAAGC
CGAAGATGAAATAGAAGACATTCAGCAAGAAATAACTGTCTTGAGTCAATGTGACAGCTC
ATATGTAACAAAATACTATGGGTCATATTTAAAGGGGTCTAAATTATGGATAATAATGGA
ATACCTGGGCGGTGGTTCAGCACTGGATCTTCTTCGAGCTGGTCCATTTGATGAGTTCCA
GATTGCTACCATGCTAAAGGAAATTTTAAAAGGTCTGGACTATCTGCATTTCAGAAAAGAA
AATTCACCGAGACATAAAAGCTGCCAATGTCTTGCTCTCAGAACAAGGAGATGTTAAACT
TGCTGATTTTGGAGTTGCTGGTCAGCTGACAGATACACAGATTAAAAGAAATACCTTTGT
GGGAACTCCATTTTGGATGGCTCCTGAAGTTATTCAACAGTCAGCTTATGACTCAAAAGC
TGACATTTGGTCATTGGGAATTACTGCTATTGAACTAGCCAAGGGAGAGCCACCTAACTC
CGATATGCATCCAATGAGAGTTCTGTTTCTTATTCCCAAAAACAATCCTCCAACCTCTTGT
TGGAGACTTTACTAAGTCTTTTAAGGAGTTTATTGATGCTTGCCTGAACAAAGATCCATC
ATTTTCGTCCTACAGCAAAAGAACTTCTGAAACACAAATTCATTGTAAAAAATTCAAAGAA
GACTTCTTATCTGACTGAACTGATAGATCGTTTTTAAGAGATGGAAGGCAGAAGGACACAG
TGATGATGAATCTGATTCCGAGGGCTCTGATTGGAATCTACCAGCAGGGAAAAACAATAC
TCATCCTGAATGGAGCTTTACCACCGTACGAAAGAAGCCTGATCCAAAGAAAGTACAGAA
TGGGGCAGAGCAAGATCTTGTGCAAACCCTGAGTTGTTTGTCTATGATAATCACACCTGC
ATTTGCTGAACTTAAACAGCAGGACGAGAATAACGCTAGCAGGAATCAGGCGATTGAAGA
ACTCGAGAAAAGTATTGCTGTGGCTGAAGCCGCCTGTCCCGGCATCACAGATAAAATGGT
GAAGAACTAATTGAAAAATTTCAAAAGTGTTGAGCAGACGAATCCCCCTAAGAACTTA
TTATTGGCTTCTGTTTCATATGGACCCAGAGAGCCCCACCAAACCTACGTCAAGATTAAC
AATGCTTAACCCATGAGCTCCATGTGCCTTTTGGATCTTTGCAACACTGAAGATTTGGAA
GAAGCTATTAACTATTTTGTGATGGCGTTTATCATTTTATATTTTGAAGGATTATTTT
GTAAGGAATAACTTTTAATACTATAGTTTCACCTGTATTCTAGTAAATGTTGAGACACCG
TTTTGCTTTTAAGTATCCCTATTTCTTAAGTTACGAGGATGAATACCTTTTACATTTTGA
TCTTTAGTTGACTCTACAGTCATGAAACATACAGGTCTTTCAAAGTCATTCTCAATATTC
AGCTTTTGTAAATTATCAAGCTTCAAAAAGCTTTTTTTTTAAAAAACAACATGCATATT
CTAAAAATGACTATTGGTGGGGAGGTGTAAATAAGTCATACCTTCTTAAAACAGAAAATT
TAAGTAAAGTCTTTTAAATGAAACCTGTAAAAGTATTGACTCTTCTACCAAGTTGGTATG
ATATTCCAGGCAGCTCAATGATTATCACATTTGAGACCCTGTGTTTGAAGCATTTACAGG
CAATGTACAGCAACAGAGGTACCTCTTGGTGTATAGTATTTACATTCTCTTTTAGGTAGA
AGAGGCAATTTTACCCTTATTTACATGGTTAGAAATTTAAAGCAAGATCATTTACCCAA

Fig. 9A

GGATAGGTGTTTGGTAATGTTGAAGGAGTTAGTCTGGCTTCATGTTTTACATCTTCAACT
AAAATCCCATACTATCTGCTTGGATTTGGAGAGCCAAAAAATAAAGCTGATTGTCATGTG
ATTAAATATCTGATCAACAGGTATGAATATAACTTAAATCAGCATATTTTTTGGCATGGTA
ATAAATTGTCCTATAAACTATTTATATATTTTTTGTTCCTTCATAATTATCACTAATAAGCA
TCAGTTTGTGTTTTTAAAAGGATATTTAAGTGAGCATTTTCTAGTTTCATATGAAAATAA
CCATAGTACAGGATGATTTCTGTCCACACAAAGGTTAAATTAGATTGCACAGTTAATTTT
CACTTATATTTATGGTACTATTATGTGGGTGATGCCTTTTTTCTTTTAAGCCCAGTACATA
TATTATGCCTGCCTAAGTTCTGAACTGGGGCTGTATTTTCAGTAGTTGTAGAATTATTGAT
ATTTAGTTTTTGATAGCTAATGTTTAAATTGTTTGGATCTGCACAGTTTGGTTTTTGCACAA
AAGTCATTTAAAAAAATCTGAGTAATTGTCAAATATTTAAAAGAAAGATATTCTTCCTGTA
AGGAATACAGTTTTTAGTCAAAGTGGCCATTACATCCTCTTTTTAATTTACATAATACAG
ATACTTGAGAAAGTTGTTGTGGTGTGTATGCCAAGAAAATTCTTTTTATTGGTGCCTAT
ATTGTAACAATTATTTTTAATGCATTGTATTTTGAAGTAACGGTTCAGTTAAATTTTTCA
CCTGCTGTGTAAC TGAAACACAATTACAGTTTATAATCATCTGTAGAAGTCTGGAGATAA
TTTTGCAACTCATGTTATGGGTAAATGAATATTTTTGTAAAAGTAAAAGCAACAAATTT
ATAAATTGATTATTTGAACTTTACAACACAATTGCATCCCAAATACAAATTGTATTGCT
TATTCATTATAGCTATTCGTCCTGTAATCTGTTTCTAGGTGAAGCATACTCCAGTGTTTT
AGGGGTTTTGAAAATAAATATTTAAATTTTCACAGTCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 2 STLK3 HUMAN

GACAGCAGCGCCGGCCCCGGCAGCTCCCGCGGCCCCGGCCCCGGCCCCGGCCCCGGCCCC
GGCGGCACAGGETGTGCGCTGGCCCATCTGCAGGGACGCGTACGAGCTGCAGGAGGTTAT
CGGCAGTGGAGCTACTGCTGTGGTTCAGGCAGCCCTATGCAAACCCAGGCAAGAACGTGT
AGCAATAAAACGGATCAACTTGGA AAAATGCCAGACCAGTATGGATGAACTATTAAAAGA
AATTCAAGCCATGAGTCAGTGCAGCCATCCCAACGTAGTGACCTATTACACCTCTTTTGT
GGTCAAAGATGAACTTTGGCTGGTCATGAAATTACTAAGTGGAGGTTCAATGTTGGATAT
CATAAAATACATTGTCAACCGAGGAGAACACAAGAATGGAGTTCTGGAAGAGGCAATAAT
AGCAACAATTCTTAAAGAGGTTTTTGAAGGCTTAGACTATCTACACAGAAACGGTCAGAT
TCACAGGGATTTGAAAGCTGGTAATATTCTTCTGGGTGAGGATGGTTCAGTACAAATAGC
AGATTTTGGGGTAAGTGC GTTCCTAGCAACAGGGGGTGATGTTACCCGAAATAAAGTAAG
AAAAACATTTCGTTGGCACCCCATGTTGGATGGCTCCTGAAGTCATGGAACAGGTGAGAGG
CTATGACTTCAAGGCTGACATGTGGAGTTTTTGAATAACTGCCATTGAATTAGCAACAGG
AGCAGCGCCTTATCACAAATATCCTCCCATGAAAGTGTTAATGTTGACTTTGCAAAATGA
TCCACCCACTTTGGAACAGGGGTAGAGGATAAAGAAATGATGAAAAAGTACGGCAAGTC
CTTTAGAAAATTACTTTCACTGTGTCTTCAGAAAGATCCTTCCAAAAGGCCACAGCAGC
AGAACTTTTAAAATGCAAATTTCTTCAGAAAGCCAAGAACAGAGAGTACCTGATTGAGAA
GCTGCTTACAAGAACACCAGACATAGCCCAAAGAGCCAAAAAGGTAAGAAGAGTTCCTGG

Fig. 9B

GTCAAGTGGTCACCTTCATAAAACCGAAGACGGGGACTGGGAGTGGAGTGACGACGAGAT
GGATGAGAAGAGCGAAGAAGGGAAAGCAGCTTTTTCTCAGGAAAAGTCACGAAGAGTAAA
AGAAGAAAATCCAGAGATTGCAGTGAGTGCCAGCACCATCCCCGAACAAATACAGTCCCT
CTCTGTGCACGACTCTCAGGGCCCCACCCAATGCTAATGAAGACTACAGAGAAGCTTCTTC
TTGTGCCGTGAACCTCGTTTTGAGATTAAGAACTCCAGAAAGGAACTTAATGACATACG
ATTTGAGTTTACTCCAGGAAGAGATACAGCAGATGGTGTATCTCAGGAGCTCTTCTCTGC
TGGCTTGGTGGATGGTCACGATGTAGTTATAGTGGCTGCTAATTTACAGAAGATTGTAGA
TGATCCCAAAGCTTTAAAAACATTGACATTTAAGTTGGCTTCTGGCTGTGATGGGTCGGA
GATTCCTGATGAAGTGAAGCTGATTGGGTTTGCTCAGTTGAGTGTGAGCTGATGTATGTC
CCTTGATGTCACCCTGATCTGTCATGCCCCACCGCCACCCCTACTCCCTTCAACCCTCCC
TCTTTCTGCCCCATTTCTCTCCACCCCTCACTCCCATTTCTAGCAAAATCAGAAGATTG
TGAAGAGGGCCGGCTTCAACAAAATGGGATAAAAAAATAATTTTTTAAACTTACAACACT
CCGAGTTCTGCTTTATTCTCTAGCAATCCACAGTACAAGAACAAGCAAATGCCACAGCTG
CACGACTGTTGCTCATTTTTTCCAAAAGCTATTTAATATTCTTAGCAATCAATTTGGATAT
CCCTTAAGTGAAAAGAATCTGAAATACACTCAGGTGGTCTTATTTATTGGCAACAAAAGG
AATTTTCTATCCAGAAGCCTATTTCTCCTTTTCAATTGTTGTTATTTCTGTTATAATACTTT
AATTGTACATCTGACAATACTGCCTCTTTTTATGTTGTATTTAGAAATTAATATACTTATA
AAATTAAGATTTATTAGCCAAACTTGAATTCTAGTTTTAAACTGACTGTGAATTTTATT
TTTCATATATTTATGCATTACACACCTTAGCTATAAGAAAAAAAGGGTTTTGATTATATG
CTTCTTGCAAGTTAATCTCGTTATTTAAACAAAAAGTTTTGGGTCTATCTTTGGAGTATTT
GTAACCTCTAAATTTTGAAATGACTGAATTAGGAATTTGGATGCTTATTCTTTTAGTCTG
TTTGCCTAAAAACCAATTTACAATCTGACTGTCTCTTGGGAGAGGGAGGTGCCTTGCAAA
CTTTCACATTAAGAATGTGCCTGAGGCTGCTTTACTCTGGAATAGTCTCAGATCTAAAT
TTCCTCTATATAAGGTGGCATATGTAAAGTTTTGCTTCATTGGACCGTTTAGAATGCTAT
GTAAAATGTTGCCATTCTGTTAGATTGCTAACTATATACCCATCTCTGATTTGGCTCTCC
TTAAGTGATAGGATTTGTTATTCTAAAGGTGATAAACTTGAAAATATCAGAATCTGAGTT
TTACTTGAAATTTTGCAGAATACCCAGGTGGAGTGAAAATTGGAAGGGTTTTGTGCAATG
ACTAAAAGGTAAAACGCTGTTAAGGTTCAAGAATCAATACTTTCAACCCAAGTAGCCCTC
TGCTTGACTGTATATTATGGAAGTAGTAAACCTTAGGATTTTGAAAATTGGAGTCTAATC
TTTCAAGGAGGTGGGCTCCCAGGATGGTACCATTGCTCTTTCTAGCTAACCTAGATAT
GGCAGCTCTTTAATGTACTTCAAAAAGCAAATATATATTAAGGAAAAAAAGTTATTT
ATAATTGCCTTGTCATAATTGTTAAGGTGTTCTAGAGCCATTTGCATACAATTTAATGTA
ATTTCAATTCCATTCTATTGTTTACACAACGATTACTCGAAGATGACTGCAAAGGTAAAAG
GAAAATAAAAGTGTATTGCACAATGAAAAA

SEQ ID NO: 3 STLK4 HUMAN

CAAAAGTGGAGTCCTAGATGANTCTACCATTGCTACGATACTCCGAGAAGTACTGGAAGG
GCTGGAATATCTGCATAAAANTGGACAGATCCACAGAGATGTGAAAGCTGGAAACATTCT

Fig. 9C
35/76

TNTTGGAGAAGATGGCTCAGTACAGATTTTCAGACTTTGGGGTTAGTGCTTTTTTTAGCAAC
TGGTGGTGATATTACCCGAAATAAAGTGAGAAAGACCTTTGTTGGCACCCCTTGTTGGAT
GGCACCTGAAGTTATGGAACAGGTCCGTGGTTATGATTTCAAAGCTGATATTTGGAGTTT
TGGAATTACAGCAATTGAATTGGCTACAGGGGCGGCTCCTTATCATAAATATCCACCAAT
GAAGGTTTTAATGCTGACACTGCAGAACGATCCTCCTTCTTTGGAAACTGGTGTTCAAGA
TAAAGAAATGCTGAAAAAATATGGAAAATCATTTAGAAAAATGATTTTCATTGTGCCTTCA
AAAAGATCCAGAAAAAAGACCAACAGCAGCAGAACTATTAAGGCACAAATTTTTCCAGAA
AGCAAAGAATAAAGAATTTCTTCAAGAAAAAACATTGCAGAGAGCACCAACCATTTCTGA
AAGAGCAAAAAAGGTTCCGGAGAGTACCAGGTTCCAGTGGGCGTCTTCATAAGACAGAGGA
TGGAGGCTGGGAGTGGAGTGATGATGAATTTGATGAAGAAAGTGAGGAAGGGAAAGCAGC
AATTTCACTACTCAGGTCTCCCCGAGTGAAAGAATCAATATCAAATTCTGAGCTCTTTCC
AACAACTGATCCTGTGGGTACTTTGCTCCAAGTTCCAGAACAGATCTCTGCTCATCTACC
TCAGCCAGCTGGGCAGATTGCTACACAGCCAACTCAAGTCTCTCTCCCACCCACCGCAGA
GCCAGCAAAAAACAGCTCAGGCTTTGTCTTCAGGATCAGGTTCAACAAGAAACCAAGATCCC
AATCAGTCTAGTACTAAGATTAAGGAATTCCAAAAAAGAACTAAATGATATTCGATTTGA
ATTTACTCCTGGGAGAGATACAGCAGAGGGTGTCTCTCAGGAACTCATTTCTGCTGGCCT
GGTCGACGGAAGGGATTTAGTAATAGTGGCAGCTAATTTGCAGAAAATTGTGGAAGAACC
TCAGTCAAATCGATCTGTCACTTTCAAAGTGGCATCTGGTGTGGAAGGCTCAGATATTCC
TGATGATGGTAAACTGATAGGATTTGCCAGCTCAGCATCAGCTAAACCACAACCCTGGA
AGAGGCGGCCTAAGGAGATTCCACACATGCGTATCTCTGTTGCTTCTATTGGCCTAAACC
CACTACTGCCAAAGAACCAGCAACAAACCTCCCGGCTAGGAGCTTTAGAAGTCTTTATG
TTCTTCCTGCCATCATTCTCTCTTTTCCACAGGGAAAGAAAAGTTGGATCACTAGTGGC
CAGCATCCCCAGAGTTCCGTTAGTAACTTACTTCATATGTCCCCTGTCTTCTCTCCATCT
GAGAAGTGGCCCATGTGCTTCAAGGCCAGGAGGGAGATCTGTCAGCTCATTCTTGCCTT
ACTCCAATGATGGCCCAGGTGGAAAAGTAGCAGCTGTATCGGGCTTCTCATCCTGCCTG
TTCCCCCACACCTGCCAGGATATGGACATCTTGGGATATCTCTTTACCACTGAAGTAGAA
TTGATTGTTTCACTGGAGCCCAGAGAATTTAATTTAATGTTTTTTCTTTGTACCTGATGT
GAATTCTAGCAACCTTTGTTAGGAAAAAGCACAGCCTCAGATGGAGGCAGCCTAAACTGT
GTTCTTGTTTTGTTTCAATGGTGTCTTAAGCGTTTTTGCTGAAGCTGCTCTCAGGCACCCCC
TTCTTCATTGCTCTCTCCAGAAAGGGTTGCTAGCCTTAACCTTCAGCTGGTGCAAAACATC
TGAAGTGTAGCCGAACCTTCAGCCATCAGATCCTTCAAAGTGGAACCTTTGGATTGTTTTTAC
AGACAACATCGAGTAATGGCTTGTAATGTGAATTTTGCCAGAGGTGGTTTTTGAACAGG
AAAATCATAATTCATATCATTGGAGAAGTATTTATTTTCAAATATCAAATTGAAGAAAAA
CTCAATCCTCCCATGAAAATCAGTTCGCCTGGCCTCCAAGTCGTGAGGAAATGGGTATGC
AAGGCTGAGATTTCTACAGCAATAAAGGAGACACACACTGGGCCAGAGAGGCCTGCCTTC
TGCCTGCTCTCCTGCACTGACCCTTTGGAGGGGGTCTCTGTGTGCTGAAGCTAACTCAAG
ATGGAAAGTGAAACCACATGTGCCGTGACCTTTAGGTTTTATGAGTAGACAGTGTTTATT
TGATTTTCTACAGAAATAATATAAATTATTCTTTAGGTTTAAAAAAGAGCACTCATAATG

Fig. 9D

36/76

CAATATGTGAATAATCAGTGAGGTTGATTTTTCTTTTTTCTACCGTTTCATAGTCTTTG
TCTAACTGCTAGTAACCTACCGAGTTTTATATATGAGTGGGATACTCAATCTGGCCTTA
AAAAGATACACAAAGATGGGCTGTGGGTCCCTGGAAAGGGGGAGAGTTGCCCTTTACAGA
ATCACTCGAGCCCTTTCCAGCACTGTTGGTCTGATGAACAAGGTTGTTTTACCTTATTTT
CTCTTGGAACATATCTGAAAACCTTCCCCACAAATAACTTGTACACCTTTTGTTCATT
CTGAGTCTTTAGTTTTAGTCATGGGCTTTCTTCACCTGCTCTAGGTGCAAAGGCATGTTG
GGAAAGAGATGGATGTTGGGGAGGAAGAGAGGAGATGGATTTTCAGTTGGGAGTTAGGAGG
AGAGTAGGTGAGATGATCAGACACCGGAGTTCAACGTCCCAGCAGTCTTGGTAAAAGGAG
GGAGCCTGCTGAGCCAGGAGGGAGAAAAGAAGATTGACCAGCTTGCTAGAAAAATACTTA
GCTTTTCTTTTTCTTTTTTTTGTGGAGGGGGGACGGAGAGGAACAAGGATGGGGAGGTAGG
AATGAGGTATAGAAAAGAGATAGCATCTTCTTTGGCACAAGACTAGTGGCTTACCGCTTA
CCTTAGAGTTTTGTTTTTTTTTTTTCAAACCCATCAAAATCTACTTATTTATGAATCCAA
GGGGTGGCAGCATCACTCTGTTCTAGCATTCTTTGTGGAGATGGTCTGGTGCCTAGCTGG
GAGTGAGCAGCAGCCCATCCCCTGTTCACTTTCTCTAGCCCATCATTACCTGTGAAGTGC
AGTGGGGCAGTCATGGCAAATAGAATTGGGCTGGGGTTTCTCCTTCTTTTCAGTTCATTG
TTTGGCCTGCTAGGAATTAGAAGACAGACACCATGTCCCAGGACAGTGTTACTTCTTCTG
CATGATGTGTGGTAGACTCCCTTTGCTGGCTTGTGCAGTGATACTGAGAAAATACATGAA
CAGAAACTGCCAGGTGGAACAGCACGTAACTAGTGAGTGACTGTACTCCTTTCTAGGA
ATGCTGATTCAGAGTGCACCTCTTTGACTAGGTCCCAGGATCCCCTTGTCCCTGGAGTAG
GGACTAACTATAGCACAAAGTAATATGTGCCAATGCTATTTGTGAAATGTTTGGTCTTTC
TAAACGACTAAAGGATTTGTTGGGTTTTTGTCTTAAGTTTTGAACCAAATCCTAGAGCCAG
CTGATAATATTTAATAATCTGGAGGAGAGAATAATGATGTACCAATAAGTGGAGATTCCT
CCTTATGATGTATGCTAGGTTATGGAAGATGTAAAATATTCAACTTTTTCTCCTTTTTT
TGGACTTTGTATTTTACTGCATGTTTTCTTCATTTTTAATCAATAAAGAGTAAATTGTCA
AAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 4 STLK5 HUMAN

CTCATCTGTACACACTTCATGGATGGCATGAATGAGCTGGCGATTGCTTACATCCTGCAG
GGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAAA
GCCAGCCACATCCTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGGCGAGCAAC
CTCAGCATGATAAGCCATGGGCAGCGGCAGCGAGTGGTCCACGATTTTCCCAAGTACAGT
GTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCTCCAGCAGAATCTCCAGGGTTATGAT
GCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCATGTC
CCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCC
TGCCTGTTGGATACCAGCACCATCCCCGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCA
GTGGCCAACTCTGGCCTGAGTGACAGCCTGACCACCAGCACCCCCCGGCCCTCCAACGGT
GACTCGCCCTCCCACCCCTACCACCGAACCTTCTCCCCCACTTCCACCACTTTGTGGAG
CAGTGCCTTCAGCGCAACCCGGATGCCAGGCCAGTGCCAGCACCTCCTGAACCACTCT

Fig. 9E
37/76

TTCTTCAAGCAGATCAAGCGACGTGCCTCAGAGGCTTTGCCCGAATTGCTTCGTCCTGT
ACCCCCATCACCAATTTTGAGGGCAGCCAGTCTCAGGACCACAGTGGAATCTTTGGCCTG
GTAACAAACCTGGAAGAGCTGGAGGTGGACGATTGGGAGTTCTGAGCCTCTGCAAACCTGT
GCGCATTCTCCAGCCAGGGATGCAGAGGGCCACCCAGAGGCCCTTCCTGAGGGCCGGCCAC
ATTCCCGCCCTCCTGGGCAGATTGGGTAGAAAGGACATTCTTCCAGGAAAGTTGACTGCT
GACTGATTGGGAAAGAAAATCCTGGAGAGATACTTCACTGCTCCAAGGCTTTTGAGACAC
AAGGGAATCTCAACAACCAGGGATCAGGAGGGTCCAAAGCCGACATTCCCAGTCCTGTGA
GCTCAGGTGACCTCCTCCGCAGAAGAGAGATGCTGCTCTGGCCCTGGGAGCTGAATTCCA
AGCCCAGGGTTTGGCTCCTTAAACCCGAGGACCGCCACCTCTTCCCAGTGCTTGCGACCA
GCCTCATTCTATTTAACTTTGCTCTCAGATGCCTCAGATGCTATAGGTCAGTGAAAGGGC
AAGTAGTAAGCTGCCTGCCTCCCTTCCCTCAGACCTCTCCCTCATAATTCCAGAGAAGGG
CATTTCTGTCTTTTTTAAGCACAGACTAAGGCTGGAACAGTCCATCCTTATCCCTCTTCTG
GCTTGGGCCCTGACACCTAAGTCTTTCCACGGTTTATGTGTGTGCCTCATTCTTTCCC
ACCAAGAATCCATCTTAGCGCCTCCTGCCAGCTGCCCTGGTGCTTTCTCCAAGGGCCATC
AGTGTCTTGCCTAGCTTGAGGGCTTAAGTCCTTATGCTGTGTTAGTTTCGTTGTCAGAAC
AAATTAATAATTTTCAGAGACGCTG

SEQ ID NO: 9 ZC1 HUMAN

GAGACCATGGCGAACGACTCTCCCGCGAAAAGTCTGGTGGACATCGACCTCTCCTCCCTG
CGGGATCCTGCTGGGATTTTTGAGCTGGTGGAAAGTGGTTGGAAATGGCACCTATGGACAA
GTCTATAAGGGTCGACATGTTAAAACGGGTCAGTTGGCAGCCATCAAAGTTATGGATGTC
ACTGAGGATGAAGAGGAAGAAATCAAACCTGGAGATAAATATGCTAAAGAAATACTCTCAT
CACAGAAACATTGCAACATATTATGGTGCTTTTCATCAAAAAGAGCCCTCCAGGACATGAT
GACCAACTCTGGCTTGTTATGGAGTTCTGTGGGGCTGGGTCCATTACAGACCTTGTTGAAG
AACACCAAAGGGAACACACTCAAAGAAGACTGGATCGCTTACATCTCCAGAGAAATCCTG
AGGGGACTGGCACATCTTCACATTCATCATGTGATTCAACGGGATATCAAGGGCCAGAAT
GTGTTGCTGACTGAGAATGCAGAGGTGAACTTGTTGACTTTGGTGTGAGTGCTCAGCTG
GACAGGACTGTGGGGCGGAGAAATACGTTTCATAGGCACTCCCTACTGGATGGCTCCTGAG
GTCATCGCCTGTGATGAGAACCCAGATGCCACCTATGATTACAGAAGTGATCTTTGGTCT
TGTGGCATTACAGCCATTGAGATGGCAGAAGGTGCTCCCCCTCTCTGTGACATGCATCCA
ATGAGAGCACTGTTTTCTCATTCCCAGAAACCTCCTCCCCGGCTGAAGTCAAAAAAATGG
TCGAAGAAGTTTTTTAGTTTTATAGAAGGGTGCCTGGTGAAGAATTACATGCAGCGGGCC
TCTACAGAGCAGCTTTTGAAACATCCTTTTATAAGGGATCAGCCAAATGAAAGGCAAGTT
AGAATCCAGCTTAAGGATCATATAGATCGTACCAGGAAGAAGAGAGGGCGAGAAAGATGAA
ACTGAGTATGAGTACAGTGGGAGTGAGGAAGAAGAGAGGAAGTGCTGAACAGGAAGGA
GAGCCAAGTTCCATTGTGAACGTGCCTGGTGAAGTCTACTCTTCGCCGAGATTTCTGAGA
CTGCAGCAGGAGAACAAGGAACGTTCCGAGGGCTCTTCGGAGACAACAGTTACTACAGGAG
CAACAGCTCCGGGAGCAGGAAGAATATAAAAGGCAACTGCTGGCAGAGAGACAGAAGCGG

Fig. 9F
38/76

ATTGAGCAGCAGAAAGAACAGAGGCGACGGCTAGAAGAGCAACAAAGGAGAGAGCGGGAA
GCTAGAAGGCAGCAGGAACGTGAACAGCGAAGGAGAGAACAAGAAGAAAAGAGGGCGTCTA
GAGGAGTTGGAGAGAAGGCGCAAAGAAGAAGAGGAGAGGAGACGGGCAGAAGAAGAAAAG
AGGAGAGTTGAAAGAGAACAGGAGTATATCAGGCGACAGCTAGAAGAGGAGCAGCGGCAC
TTGGAAGTCCTTCAGCAGCAGCTGCTCCAGGAGCAGGCCATGTTACTGGAGTGCCGATGG
CGGGAGATGGAGGAGCACCGGCAGGCAGAGAGGCTCCAGAGGCAGTTGCAACAAGAACAA
GCATATCTCCTGTCTCTACAGCATGACCATAGGAGGGCCGCACCCGCAGCACTCGCAGCAG
CCGCCACCACCGCAGCAGGAAAGGAGCAAGCCAAGCTTCCATGCTCCCGAGCCCCAAAGCC
CACTACGAGCCTGCTGACCGAGCGCGAGAGGTGGAAGATAGATTTAGGAAAACCTAACCAC
AGCTCCCCCTGAAGCCCAGTCTAAGCAGACAGGCAGAGTATTGGAGCCACCAGTGCCTTCC
CGATCAGAGTCTTTTTCCAATGGCAACTCCGAGTCTGTGCATCCCGCCCTGCAGAGACCA
GCGGAGCCACAGGTTCTCTGTGAGAACAAACATCTCGCTCCCTGTTCTGTCCCGTCGAGAT
TCCCCACTGCAGGGGCAGTGGGCAGCAGAATAGCCAGGCAGGACAGAGAACTCCACCAGT
ATTGAGCCCAGGCTTCTGTGGGAGAGAGTGGAGAAGCTGGTGCCCAGACCTGGCAGTGGC
AGCTCCTCAGGGTCCAGCAACTCAGGATCCCAGCCCCGGGTCTCACCTGGGTCTCAGAGT
GGCTCCGGGGAAACGCTTCAGAGTGAGATCATCATCCAAGTCTGAAGGCTCTCCATCTCAG
CGCCTGGAAAATGCAGTGAAAAAACCTGAAGATAAAAAGGAAGTTTTTCAGACCCCTCAAG
CCTGCTGATCTGACCGCACTGGCCAAAGAGCTTCGAGCAGTGGAAGATGTACGGCCACCT
CACAAAGTAACGGACTACTCCTCATCCAGTGAGGAGTCGGGGACGACGGATGAGGAGGAC
GACGATGTGGAGCAGGAAGGGGCTGACGAGTCCACCTCAGGACCAGAGGACACCAGAGCA
GCGTCATCTCTGAATTTGAGCAATGGTGAAACGGAATCTGTGAAAACCATGATTGTCCAT
GATGATGTAGAAAGTGAGCCGGCCATGACCCCATCCAAGGAGGGCACTCTAATCGTCCGC
CGGACTCAGTCCGCTAGTAGCACACTCCAGAAACACAAATCTTCCTCCTCCTTTACACCT
TTTATAGACCCCAGATTACTACAGATTTCTCCATCTAGCGGAACAACAGTGACATCTGTG
GTGGGATTTTCTGTGATGGGATGAGACCAGAAGCCATAAGGCAAGATCCTACCCGGAAA
GGCTCAGTGGTCAATGTGAATCCTACCAACACTAGGCCACAGAGTGACACCCCGGAGATT
CGTAAATACAAGAAGAGGTTTAACTCTGAGATTCTGTGTGCTGCCTTATGGGGAGTGAAT
TTGCTAGTGGGTACAGAGAGTGGCCTGATGCTGCTGGACAGAAGTGGCCAAGGGAAGGTC
TATCCTCTTATCAACCGAAGACGATTTCAACAAATGGACGTAATTGAGGGCTTGAATGTC
TTGGTGACAATATCTGGCAAAAAGGATAAGTTACGTGTCTACTATTTGTCTGTTAAGA
AATAAAATACTTCACAATGATCCAGAAGTTGAGAAGAAGCAGGGATGGACAACCGTAGGG
GATTTGGAAGGATGTGTACATTATAAAGTTGTAAAATATGAAAGAATCAAATTTCTGGTG
ATTGCTTTGAAGAGTTCTGTGGAAGTCTATGCGTGGGCACCAAAGCCATATCACAAATTT
ATGGCCTTTAAGTCATTTGGAGAATTGGTACATAAGCCATTACTGGTGGATCTCACTGTT
GAGGAAGGCCAGAGGTTGAAAGTGATCTATGGATCCTGTGCTGGATTCCATGCTGTTGAT
GTGGATTCAAGGATCAGTCTATGACATTTATCTACCAACACATATCCAGTGTAGCATCAAA
CCCCATGCAATCATCATCCTCCCCAATACAGATGGAATGGAGCTTCTGGTGTGCTATGAA
GATGAGGGGGTTTATGTAAACACATATGGAAGGATCACCAAGGATGTAGTTCTACAGTGG

Fig. 9G
39/76

GGAGAGATGCCTACATCAGTAGCATATATTCGATCCAATCAGACAATGGGCTGGGGAGAG
AAGGCCATAGAGATCCGATCTGTGGAACTGGTCACTTGGATGGTGTGTTTCATGCACAAA
AGGGCTCAAAGACTAAAATTCTTGTGTGAACGCAATGACAAGGTGTTCTTTGCCTCTGTT
CGGTCTGGTGGCAGCAGTCAGGTTTATTTTCATGACCTTAGGCAGGACTTCTCTTCTGAGC
TGGTAGAAGCAGTGTGATCCAGGGATTACTGGCCTCCAGAGTCTTCAAGATCCTGAGAAC
TTGGAATTCCTTGTAAC

SEQ ID NO: 10 ZC2 HUMAN

GCTTTCGGGGAGGTCTATGAGGGTCGTCATGTCAAAACGGGGCCAGCTTGCAGCCATCAAG
GTTATGGATGTCACAGGGGATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAG
AAATATTCTCATCACCGGAATATTGCTACATACTATGGTGCTTTTATCAAAAAGAACCCA
CCAGGCATGGATGACCAACTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACC
GACCTGATCAAGAACACAAAAGGTAACACGTTGAAAGAGGAGTGGATTGCATACATCTGC
AGGGAAATCTTACGGGGGCTGAGTCACCTGCACCAGCATAAAGTGATTTCATCGAGATATT
AAAGGGCAAAATGTCTTGCTGACTGAAAATGCAGAAGTTAACTAGTGGACTTTGGAGTC
AGTGCTCAGCTTGATCGAACAGTGGGCAGGAGGAATACTTTTCATTGGAACCTCCTACTGG
ATGGCACCAGAAGTTATTGCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGT
GACTTGTGGTCTTTGGGTATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGT
GACATGCACCCCATGAGAGCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAG
TCTAAGAAGTGGTCAAAAAAATTCCAGTCATTTATTGAGAGCTGCTTGGTAAAGAATCAC
AGCCAGCGACCAGCAACAGAACAATTGATGAAGCATCCATTTATACGAGACCAACCTAAT
GAGCGACAGGTCCGCATTCAACTCAAGGACCATATTGATAGAACAAGAAGAGAGGAGGA
GAAAAAGATGAGACAGAGTATGAGTACAGTGGAGTGGAGGAAGAAGAGGAGGAGAATGAC
TCAGGAGAGCCCAGCTCCATCCTGAATCTGCCAAGGGAGTCGACGCTGCGGAGGGACTTT
CTGAGGCTGCAGCTGGCCAACAAGGAGCGTTCTGAGGCCCTACGGAGGCAGCAGCTGGAG
CAGCAGCAGCGGGAGAATGAGGAGCACAAGCGGCAGCTGCTGGCCGAGCGTCAGAAGCGC
ATCGAGGAGCAGAAAGAGCAGAGGCGGCGGCTGGAGGAGCAACAAAGGCGAGAGAAGGAG
CTGCGGAAGCAGCAGGAGAGGGAGCAGCGCCGGCACTATGAGGAGCAGATGCGCCGGGAG
GAGGAGAGGAGGCGTGCGGAGCATGAACAGGAATATAAGCGCAAACAATTGGAAGAACAG
AGACAAGCAGAAAGACTGCAGAGGCAGCTAAAGCAAGAAAGAGACTACTTAGTTTTCCCTT
CAGCATCAGCGGCAGGAGCAGAGGCCTGTGGAGAAGAAGCCACTGTACCATTACAAGAA
GGAATGAGTCCTAGTGAGAAGCCAGCATGGGCCAAGGAGGTAGAAGAACGGTCAAGGCTC
AACCGGCAAAAGTTCCCCTGCCATGCCTCACAAGGTTGCCAACAGGATATCTGACCCCAAC
CTGCCCCCAAGGTCGGAGTCCTTCAGCATTAGTGGAGTTCAGCCTGCTCGAACACCCCCC
ATGCTCAGACCAGTCGATCCCCAGATCCCACATCTGGTAGCTGTAAAATCCCAGGGACCT
GCCTTGACCGCCTCCAGTCAGTGCACGAGCAGCCCACAAAGGGCCTCTCTGGGTTTCAG
GAGGCTCTGAACGTGACCTCCACCGCGTGGAGATGCCACGCCAGAAGTCAAGATCCCACC
TCGGAAAATCCTCCTCTCCCCACTCGCATTGAAAAGTTTGACCGAAGCTCTTGGTTACGA

CAGGAAGAAGACATTCCACCAAAGGTGCCTCAAAGAACAACCTTCTATATCCCCAGCATTAGCCAGAAAGAATTCTCCTGGGAATGGTAGTGCTCTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCAACCCTGATCTCCGGAGAACTGAGCCCATCTTGAGAGAGCCCCTTGCAGAGGACCAGCAGTGGCAGTTCCTCCAGCTCCAGCACCCCTAGCTCCCAGCCCAGCTCCCAAAGGAGCTCCCAGCCTGGATCACAAAGCAGGATCCAGTGAACGCACCAGAGTTCGAGCCAAACAGTAAGTCAGAAGGATCACCTGTGCTCCCCCATGAGCCTGCCAAGGTGAAACCAGAAGAAATCCAGGGACATTACCCGGCCCCAGTCGACCAGCTAGCTACAAAAAAGCTATAGATGAGGATCTGACGGCATTAGCCAAAGAACTAAGAGAACTCCGGATTGAAGAAAACAAACCGCCCAATGAAGAAGGTGACTGATTACTCCTCCTCCAGTGAGGAGTCAGAAAGTAGCGAGGAAGAGGGAGGAAGATGGAGAGAGCGAGACCCATGATGGGACAGTGGCTGTCAGCGACATACCCAGACTGATACCAACAGGAGCTCCAGGCAGCAACGAGCAGTACAATGTGGGAATGGTGGGGACGCATGGGCTGGAGACCTCTCATGCGGACAGTTTCAGCGGCAGTATTTCAAGAGAAGGAACCTTGATGATTAGAGAGACGTCTGGAGAGAAGAAGCGATCTGGCCACAGTGACAGCAATGGCTTGGCTGGCCACATCAACCTCCCTGACCTGGTGCAGCAGAGCCATTCTCCAGCTGGAACCCCGACTGAGGGACTGGGGCGCGTCTCAACCCATTCCCAGGAGATGGACTCTGGGACTGAATATGGCATGGGGAGCAGCAACCAAAGCCTCCTTCACCCCTTTGTGGACCCAGAGTATACCAGACGTCTCCCCTGATGAAGATGAAGAGGATGAGGAATCATCAGCCGCAGCTCTGTTTACTGGCGAACTTCTTAGGCAAGAACAGGGCCAACTCAATGAAGCAAGAAAGATTTTCGGTGGTAATGTAAACCCCAACCAACATTTCGGCCTCATAGCGACACACCAGAAATCAGAAAATACAAGAAACGATTCAACTCAGAAATACTTTGTGCAGCTCTGTGGGGTGTAACCTTCTGGTGGGGACTGAAAATGGCCTGATGCTTTTTGGACCGAAGTGGGCAAGGCAAAGTCTATAATCTGATCAACCGGAGGCGATTTTCAGCAGATGGATGTGCTAGAGGGACTGAATGTCCTTGTGACAATTTCAGGAAAGAAGAATAAGCTACGAGTTTACTATCTTTCATGGTTAAGAAACAGAATACTACATAATGACCCAGAAGTAGAAAAGAAACAAGGCTGGATCACTGTTGGGGACTTGGAAGGCTGTATACATTATAAAGTTGTTAAATATGAAAGGATCAAATTTTTGGTGATTGCCTTAAAGAATGCTGTGGAAATATATGCTTGGGCTCCTAAACCGTATCATAAATTCATGGCATTTAAGTCTTTTGCAGATCTCCAGCACAAAGCCTCTGCTAGTTGATCTCACGGTAGAAGAAGGTCAAAGATTAAAGGTTATTTTTGGTTCACACACTGGTTTCCATGTAATTGATGTTGATTCAGGAACCTCTTATGATATCTACACACCATCTCATATTCAGGGCAATATCACTCCTCATGCTATTGTCATCTTGCCTAAAACAGATGGAATGGAAATGCTTGTTTGCTATGAGGATGAGGGGGTG TATGTAAACACCTATGGCCGGATAACTAAGGATGTGGTGCTCCAATGGGGAGAAATGCCCACGTCTGTGGCCTACATTCAATCCAATCAGATAATGGGCTGGGGCGAGAAAGCTATTGAGATCCGGTCAGTGGAAACAGGACATTTGGATGGAGTATTTATGCATAAGCGAGCTCAAAGGTTAAAGTTTCTATGTGAAAGAAATGATAAGGTATTTTTTGCATCCGTGCGATCTGGAGGAAGTAGCCAAGTGTTTTTTCATGACCCTCAACAGAAATTCATGATGAACTGGTAACAGAAGAGCACTTGGCACTTATCTTCATGGCGTTATTTCTAATTTAAAGAACATAACTCATGTGGACTTATGCCAGTCTAGAGGCAGAATCAGAAGGCTTGGTTGAACATATCGCTTTCCTTTTTCCTCTCCCTCCGCCCCCTCCCAGTACAGTCCATCT

Fig. 9 I
41/76

SEQ ID NO: 11 ZC3 HUMAN

GCATTTGGGGAGGTGTATGAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAG
GTCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAA
AAGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCC
CCGGGAAACGATGACCAGCTCTGGCTGGTGTATGGAGTTCTGTGGTGCTGGTTCAGTGACT
GACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGC
AGGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCCACAAGGTGATCCATCGAGACATC
AAGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTG
AGTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGG
ATGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGT
GATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCTCTGTGT
GACATGCACCCCATGCGAGCCCTCTTCCTCATTCCCTCGGAACCCTCCGCCCAGGCTCAAG
TCCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTAC
CTGAGCCGCCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACG
GAGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGT
GAGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGA
GAGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAG
TTTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAG
CTGCAGCAGCAGCAGCAGCAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGG
CAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGG
GAGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAG
GCTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCGTAC
AGGCTAGAGGAGGAGCAGCGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAG
GCCCTGCTGCTGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTC
CAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAG
CAGCAGCTTCAGAAACAACAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTAC
CATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCCGAGAGGTAGAAGAG
AGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACG
GGGCCTGAGCCCCCATCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCAGACT
CCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAAGAGCCTGGTGGCACAC
CGGGTCCCACTGAAGCCATATGCAGCACCTGTACCCCGATCCCACTCCCTGCAGGACCAG
CCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCA
CCCACTGCCACGCCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACTCT
GAAGGACCTGGCCCCAGCCCGAATCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCA
CCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGA
GGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATC
TATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCC
CCTGGCCCCGCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAA

Fig. 9J
42/76

CGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAG
CGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAAT
AAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTG
AAAGAGCGGACTCTGGACGAGGCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCG
TCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCCGAAGGCCGGGCCAGCA
GAGGGGAGCAGAGATACCCCTGGGGGCGCGATGGGGATACAGACAGCGTCAGCACCATG
GTGGTCCACGACGTGAGGAGATCACCGGGACCCAGCCCCCATAAGGGGGCGGCACCATG
GTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTAC
ACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAA
AGCCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCT
GGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGG
GACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGGCACTCGGCTCGACCAGCTGCAG
TACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCACAGT
GAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCC
CTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGT
GGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTG
GAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAACTGCGGGTGTATTAC
TTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGC
TGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTGTGAAATACGAGCGG
ATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGGCCCCAAA
CCCTACCACAAATTTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCACCGCCCTCTGCTG
GTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGC
TTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATC
CAGAGCCAGATCACGCCCCATGCCATCATCTTCTCCCAACACCGACGGCATGGAGATG
CTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAGGAT
GTGGTGTGCTGAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATA
ATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGG
GTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTG
TTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGT
AACCGCATCATGAACTGGTGACGGGGCCCTGGGCTGGGGCTGTCCACACTGGACCCAGC
TCTCCCCCTGCAGCCAGGCTTCCCGGGCCGCCCTCTTTCCCTCCCTGGGCTTTTGCTT
TACTGGTTTGATTTCACTGGAGCCTGCTGGGAACGTGACCTCTGACCCCTGA

SEQ ID NO: 12 ZC4 HUMAN

CAATGTAAACCCACTCTATGTCTCTCCTGCATGTAAAAAACCACTAATCCACATGTATGA
AAAGGAGTTCACCTCTGAGATCTGCTGTGGTTCTTTGTGGGGAGTCAATTTGCTGTTGGG
AACCCGATCTAATCTATATCTGATGGACAGAAGTGGAAGGCTGACATTACTAACTTAT
AAGGCGAAGACCATTCCGCCAGATTCAAGTCTTAGAGCCACTCAATTTGCTGATTACCAT

Fig. 9K
43/76

CTCAGGTCATAAGAACAGACTTCGGGTGTATCATCTGACCTGGTTGAGGAACAAGATTTT
GAATAATGATCCAGAAAGTAAAAGAAGGCAAGAAGAAATGCTGAAGACAGAGGAAGCCTG
CAAAGCTATTGATAAGTTAACAGGCTGTGAACACTTCAGTGTCTCCAACATGAAGAAAC
AACATATATTGCAATTGCTTTGAAATCATCAATTCACCTTTATGCATGGGCACCAAAGTC
CTTTGATGAAAGCACTGCTATTAAAGTATTTCCAACACTTGATCATAAGCCAGTGACAGT
TGACCTGGCTATTGGTTCTGAAAAAAGACTAAAGATTTTCTTCAGCTCAGCAGATGGATA
TCACCTCATCGATGCAGAATCTGAGGTTATGTCTGATGTGACCCTGCCAAAGAATCCCCCT
GGAAATCATTATACCACAGAATATCATCATTTTACCTGATTGCTTGGGAATTGGCATGAT
GCTCACCTTCAATGCTGAAGCCCTCTCTGTGGAAGCAAATGAACAACCTCTTCAAGAAGAT
CCTTGAAATGTGGAAAGACATAACCATCTTCTATAGCTTTTGAATGTACACAGCGAACCAC
AGGATGGGGCCAAAAGGCCATTGAAGTGCGCTCTTTGCAATCCAGGGTTCTGGAAAGTGA
GCTGAAGCGCAGGTCAATTAAGAAGCTGAGATTCTGTGCACCCGGGGTGACAAGCTGTT
CTTTACCTCTACCCTGCGCAATCACCACAGCCGGGTTTACTTCATGACACTTGGAAAAC
TGAAGAGCTCCAAAGCAATTATGATGTCTAAAAGTTTCCAGTGATTTATTACCACATTAT
AAACATCATGTATAGGCAGTCTGCATCTTCAGATTTTCAGAGATTAAATGAGTATTCAGTT
TTATTTTTAGTAAAGATTAAATCCAAAACCTTTACTTTTAATGTAGCACAGAATAGTTTTA
ATGAGAAATGCAGCTTTATGTATAAAATTAAGTATAGCAAGCTCTAGGTACTCCAATGGT
GTACAATGTCTTTTGACAAACTTTGTAACCTTTTGTTACTGTGAATTCAAACATTACTCT
TTGGACAGTTTGGACAGTATCTGTATTTCAGATTTTACAACATGGAGTAAAGAAACCTGTT
ATGAATTAGATTACAAGCAGCCTTCAAAGAATTGGCACTGGGATAAGATTTTTCAGAAA
AGAAAAACATCGGCCAACT

SEQ ID NO: 17 KHS2 HUMAN

CCGCCATGAACCCCGGCTTCGATTTGTCCCGCCGGAACCCGCAGGAGGACTTCGAGCTGA
TTCAGCGCATCGGCAGCGGCACCTACGGCGACGTCTACAAGGCACGGAATGTTAACACTG
GTGAATTAGCAGCAATTAAAGTAATAAAATTGGAACCAGGAGAAGACTTTGCAGTTGTGC
AGCAAGAAATTATTATGATGAAAGACTGTAAACACCCAAATATTGTTGCTTATTTTGGAA
GCTATCTCAGGCGAGATAAGCTTTGGATTTGCATGGAGTTTTGTGGAGGTGGTTCTTTAC
AGGATATTTATCACGTAAGTGGACCTCTGTCAGAACTGCAAATTGCATATGTTAGCAGAG
AAACACTGCAGGGATTATATTATCTTCACAGTAAAGGAAAAATGCACAGAGATATAAAGG
GAGCTAACATTCTATTAACGGATAATGGTCATGTGAAATTGGCTGATTTTGGAGTATCTG
CACAGATAACAGCTACAATTGCCAAACGGAAGTCTTTCATTGGCACACCATATTGGATGG
CTCCAGAAGTTGCAGCTGTTGAGAGGAAGGGGGTTACAATCAACTCTGTGATCTCTGGG
CAGTGGGAATCACTGCCATAGAACTTGCAGAGCTTCAGCCTCCTATGTTTGAATTACACC
CAATGAGAGCATTATTTCTAATGACAAAAAGCAATTTTCAGCCTCCTAACTAAAGGATA
AAATGAAATGGTCAAATAGTTTTTCATCACTTTGTGAAAATGGCACTTACCAAAAATCCGA
AAAAAAGACCTACTGCTGAAAAATTATTACAGCATCCTTTTGTAAACACAACATTTGACAC
GGTCTTTGGCAATCGAGCTGTTGGATAAAGTAAATAATCCAGATCATTCCACTTACCATG

ATTTTCGATGATGATGATCCTGAGCCTCTTGTTGCTGTACCACATAGAATTCACTCAACAA
GTAGAAACGTGAGAGAAGAAAAACACGCTCAGAGATAACCTTTGGCCAAGTGAAATTTG
ATCCACCCTTAAGAAAGGAGACAGAACCACATCATGAACTTCCCGACAGTGATGGTTTTT
TGGACAGTTCAGAAGAAATATACTACACTGCAAGATCTAATCTGGATCTGCAACTGGAAT
ATGGACAAGGACACCAAGGTGGTTACTTTTTAGGTGCAACAAGAGTCTTCTCAAGTCTG
TTGAAGAAGAATTGCATCAGCGAGGACACGTGCGACATTTAGAAGATGATGAAGGAGATG
ATGATGAATCTAAACACTCAACTCTGAAAGCAAAAATTCCACCTCCTTTGCCACCAAAAGC
CTAAGTCTATCTTCATACCACAGGAAATGCATTCTACTGAGGATGAAAATCAAGGAACAA
TCAAGAGATGTCCCATGTCAGGGAGCCCAGCAAAGCCATCCCAAGTTCCACCTAGACCAC
CACCTCCCAGATTACCCCCACACAAACCTGTTGCCTTAGGAAATGGAATGAGCTCCTTCC
AGTTAAATGGTGAACGAGATGGCTCATTATGTCAACAACAGAATGAACATAGAGGCACAA
ACCTTTCAAGAAAAGAAAAGAAAGATGTACCAAAGCCTATTAGTAATGGTCTTCTCCAA
CACCTAAAGTGCATATGGGTGCATGTTTTTCAAAAGTTTTTAATGGGTGTCCCTTGAAAA
TTCCTGTGCATCATCATGGATAAACCCAGATACAAGAGATCAGTACTTGATATTTGGTG
CCGAAGAAGGGATTTATACCCTCAATCTTAATGAACTTCATGAAACATCAATGGAACAGC
TATTCCTCGAAGGTGTACATGGTTGTATGTAATGAACAATTGCTTGCTATCAATATCTG
GTAAAGCTTCTCAGCTTTATTCCCATAATTTACCAGGGCTTTTTTGATTATGCAAGACAAA
TGCAAAAGTTACCTGTTGCTATTCCAGCACACAAACTCCCTGACAGAATACTGCCAAGGA
AATTTTCTGTATCAGCAAAAATCCCTGAAACCAAATGGTGCCAGAAGTGTTGTGTTGTAA
GAAATCCTTACACGGGCCATAAATACCTATGTGGAGCACTTCAGACTAGCATTGTTCTAT
TAGAATGGGTTGAACCAATGCAGAAATTTATGTTAATTAAGCACATAGATTTTCTTATAC
CATGTCCACTTAGAATGTTTGAAATGCTGGTAGTTCCTGAACAGGAGTACCCTTTAGTTT
GTGTTGGTGTGAGTAGAGGTAGAGACTTCAACCAAGTGGTTGATTTGAGACGGTCAATC
CAAATTCTACCTCTTCATGGTTTACAGAATCAGATACCCACAGACAAATGTTACTCATG
TAACCCAACTGGAGAGAGATAACCATCCTTGATGCTTGGACTGTTGTATAAAAATAGTAA
ATCTCCAAGGAAGATTAAAATCTAGCAGGAAATTGTCATCAGAACTCACCTTTGATTTCC
AGATTGAATCAATAGTGTGCCTACAAGACAGTGTGCTAGCTTTCTGGAAACATGGAATGC
AAGGTAGAAGTTTTAGATCTAATGAGGTAACACAAGAAATTTAGATAGCACAGAATTT
TCAGGCTGCTTGGATCTGACAGGGTCGTGGTTTTGGAAAGTAGGCCAACTGATAACCCCA
CAGCAAATAGCAATTTGTACATCCTGGCGGGTCATGAAAACAGTTACTGAGAATTGTTGT
GCTTTGACAGTTAACTCTAGAAAGAAAGAACTACCACTGCAACATTAATGGATGCTTG
AAGCTGTACAAAAGCTGCAGTAACCTGTCTTCAGTTACTTTGTAATTTATTGTGGCATGA
GATAAGATGGGGAAAATTTTGTTTTAAAGTGGTATGGATATATTTAGCATATTGAACCACA
CAAGTGCTTAATTCATTGTTATGTAATCTTTGTACATATAGGCAGTATTTTTCTGTGAA
ACTTCATATTGCTGAAGACATACACTAAGAATTTATGTAGATAATGTACTTTTATGAGAT
GTACAAGTAAGTGTCTTATCTGTACAGATGTAAATGTTGATGAAAATGCAATTGGGGTTA
ATATTTTAAAGAATCTTTAGTATATTCTTGGGTGTGGCTATATTACAAAATGGGATGCTG
GCAATGAAACAATACATTTAACACTATTGTATTTTTATTATATGTAATTTAGTAATATGA

Fig. 9M
45/76

ATATAAATCTTGTAACCTTTTAAAATTGTAATGGAGGCTGTAATCATTTTTATAATCTTTTT
AATTTTAATGCAAGTACACTGGTGTTTATATTTGCACAAAGTATTGATATGTGATGTATT
AAGTCACAAAAGTAAGCTGTGACATTGTCTATAAGCATTGCTCCACAAATGTATTTGG
ATTGTTTTCTATGTGAAGCAAACCAATTATAATTAACCACATGTTGTAGTAACTGGTCTT
TTTATATTTAAGCAGAATCCTGTAAGATTGCTTGTCTTTGCTTAAAAACAATACCTTTGA
ACATTTTTGAATCACAGAATAGCGGTACCATGATAGAATACTGCAATTGTGGTCAGAATT
ACAGTATGCACAAAGAATTAATTAGCATTATTAAGAGAGTCTCACTAAACATTTTCATATG
ATCACACTGAAGAACTGTAACATTCCATAGAGTGAAGTGGTTCAAATTTCTCTTGGAATT
TTTACTTTTGTGCGCTTATTTTATGATCCTTTTCATATTTCTTTTGACTTAGAGTATTA
ATACATGGCCAAAATAATTTAGTTACTACCTCATACAAACAATATAATGGTTACTACACA
TCACAGGAACCTTAGTTTTGGTTTAAGTCATTTTTTGATTGCTTTTTTCCAATGGAATATGT
ATATACCAGGTTTTAGCAAAATGCACACTTTTGGCTCTTTTTGGTATATGTTCTTTATAT
TTTAATGTGAGTATATACACTAAGAACAACTAAATTGTGATTTATGATCTTCATTTATT
TTAATGATAATGGTTTTAAAATATGTTCTGATTGTACATATTGTAAAATAAACATGTTT
TTT

SEQ ID NO: 19 SULU1 HUMAN

GGGAGGGTCCTTGTGGCGCCGGGCGGGGTCCTGCGTGGAGAGTGGGACGCAACGCCG
AGACCGCGAGCAGAGGCTGCGCACAGCCGGATCCGGCACTCAGCGACCGGACCCAAGGAT
CCGCCGGGGAACAAGCCACAGGAGAGCGACTCAGGAACAAGTGTGGGAGAGGAAGCGGCG
GCGGCGGCGCCGGGCCCCGGGGGTGGTGACAGCAGGTCTGAGGTTGCATCATAAATACAAA
GGACTGAAGTTATAAAAAGAGAAAAGAGAAGTTTGCTGCTAAAATGAATCTGAGCAATATG
GAATATTTTTGTGCCACACACAAAAAGGTACTGAAGATTTACCCCCCAAAAAAATTGTCA
ATGAGAAATAAAGCTAACTGATATCAAAAAGCAGAGCCTGCTCTACTGGCCATCATGCGT
AAAGGGGTGCTGAAGGACCCAGAGATTGACGATCTATTCTACAAAGATGATCCTGAGGAA
CTTTTTATTGTTTTGCATGAAATTGGACATGGAAGTTTTGGAGCAGTTTATTTTGCTACA
AATGCTCACACCAATGAGGTGGTGGCAATTAAGAAGATGTCCTATAGTGGGAAGCAGACC
CATGAGAAATGGCAAGATATTCTTAAGGAAGTTAAATTTTTACGACAATTGAAGCATCCT
AATACTATTGAGTACAAAGGCTGTTACTTGAAAGAACACACTGCTTGGTTGGTGATGGAA
TATTGCTTAGGCTCAGCCTCTGATTTATTAGAAGTTCATAAAAAACCACTTCAGGAAGTG
GAGATCGCTGCCATTACTCATGGAGCCTTGCATGGACTAGCCTACCTACATTCTCATGCA
TTGATTCATAGGGATATTAAAGCAGGAAATATTCTTCTAACAGAGCCAGGTGAGGTAAAA
CTAGCTGATTTTGGATCTGCTTCAATGGCTTCTCCTGCCAACTCCTTCGTGGGCACACCT
TACTGGATGGCTCCAGAGGTGATCTTAGCTATGGATGAAGGACAGTATGATGGGAAAGTT
GATATTTGGTCACTTGGCATCACTTGTATTGAATTGGCGGAACGGAAGCCGCCCTTTTC
AACATGAATGCAATGAGTGCCTTATATCACATTGCCCAGAATGACTCCCCAACGTTACAG
TCTAATGAATGGACAGACTCCTTTAGGAGATTTGTTGATTACTGCTTGCAGAAAATACCT
CAGGAAAGGCCAACATCAGCAGAACTATTAAGGCATGACTTTGTTCGACGAGACCGGCCA

Fig. 9N

46/76

CTACGTGTCCTCATTGACCTCATAACAGAGGACAAAAGATGCAGTTCGTGAGCTAGATAAC
CTACAGTACCGAAAAATGAAAAAAATACTTTTCCAAGAGACACGGAATGGACCCTTGAAT
GAGTCACAGGAGGATGAGGAAGACAGTGAACATGGAACCAGCCTGAACAGGGAAATGGAC
AGCCTGGGGCAGCAACCATTCCATTCCAAGCATGTCCGTGAGCACAGGCAGCCAGAGCAGC
AGTGTGAACAGCATGCAGGAAGTCATGGACGAGAGCAGTTCCGAACCTTGTCATGATGCAC
GATGACGAAAGCACAATCAATTCCAGCTCCTCCGTGCGTGCATAAGAAAGATCATGTATTC
ACAAGGGATGAGGCGGGCCACGGCGATCCCAGGCCTGAGCCGCGGCCTACCCAGTCAGTT
CAGAGCCAGGCCCTCCACTACCGGAACAGAGAGCGCTTTGCCACGATCAAATCAGCATCT
TTGGTTACACGACAGATCCATGAGCATGAGCAGGAGAACGAGTTGCGGGAAACAGATGTCA
GGTTATAAGCGGATGCGGCGCCAGCACCAGAAGCAGCTGATCGCCCTGGAGAACAAAGCTG
AAGGCTGAGATGGACGAGCACCGCCTCAAGCTACAGAAGGAGGTGGAGACGCATGCCAAC
AACTCGTCCATCGAGCTGGAGAAGCTGGCCAAGAAGCAAGTGGCTATCATAGAAAAGGAG
GCAAAGGTAGCTGCAGCAGATGAGAAGAAGTTCCAGCAACAGATCTTGCCCCAGCAGAAG
AAAGATTTGACAACTTTCTTAGAAAGTCAGAAGAAGCAGTATAAGATTTGTAAGGAAAAA
ATAAAAGAGGAAATGAATGAGGACCATAGCACACCCAAGAAAGAGAAGCAAGAGCGGATC
TCCAAACATAAAGAGAACTTGCAGCACACACAGGCTGAAGAGGAAGCCCACCTTCTCACT
CAACAGAGACTGTACTACGACAAAAATTGTCGTTTTCTTCAAGCGGAAAATAATGATCAAG
CGGCACGAGGTGGAGCAGCAGAACATTCGGGAGGAACTAAATAAAAAGAGGACCCAGAAG
GAGATGGAGCATGCCATGCTAATCCGGCACGACGAGTCCACCCGAGAGCTAGAGTACAGG
CAGCTGCACACGTTACAGAAGCTACGCATGGATCTGATCCGTTTACAGCACCCAGACGGAA
CTGGAAAACCAGCTGGAGTACAATAAGAGGCGAGAAAGAGAACTGCACAGAAAGCATGTC
ATGGGACTTCGGCAACAGCCAAAAAACTTAAAGGCCATGGAAATGCAAATTAAAAAACAG
TTTCAGGACACTTGCAAAGTACAGACCAAACAGTATAAAGCACTCAAGAATCACCAGTTG
GAAGTTACTCCAAAGAATGAGCACAAAACAATCTTAAAGCACTGAAAGATGAGCAGACA
AGAAAACCTTGCCATTTTGGCAGAGCAGTATGAACAGAGTATAAATGAAATGATGGCCTCT
CAAGCGTTACGGCTAGATGAGGCTCAAGAAGCAGAATGCCAGGCCTTGAGGCTACAGCTC
CAGCAGGAAATGGAGCTGCTCAACGCCTACCAGAGCAAAATCAAGATGCAAACAGAGGCA
CAACATGAACGTGAGCTCCAGAAGCTAGAGCAGAGAGTGTCTCTGCGCAGAGCACACCTT
GAGCAGAAGATTGAAGAGGAGCTGGCTGCCCTTCAGAAGGAACGCAGCGAGAGAATAAAG
AACCTATTGGAAAGGCAAGAGCGAGAGATTGAAACTTTTGACATGGAGAGCCTCAGAATG
GGATTTGGGAATTTGGTTACATTAGATTTTCTAAGGAGGACTACAGATGAGATTAAATT
TTTTGCCATTTACAAAAAAGAAAAAAGAAAAACAGAAAAAATTCAGACCCTGCAA
AACCACATTCCCCATTTTAACGGGCGTTGCTCTCACTCTCTCTCTCTTACTCTTACTG
ACATCGTGTCGGACTAGTGCTGTTTATTCTTACTCCATCAGGGGCCCCCTTCTCCCCC
CGTGTCAACTTTTCAAGTGCTGGCCAAAACCTGGCCGTCTCTTCTATTACAGTACACGTCA
CAGTATTGATGTGATTCAAAATGTTTCAGTGAAAACCTTTGGAGACAGTTTTTAACAAAACC
AATAAACCAACAACAAAAAAAGTGGATGTATATTGCTTTAAGCAATCACTCATTACCACC
AATCTGTGAAAGTAAAGCAAAAAATAATAATAATAATGCCAAGGGGGAGAGAGACACAA

TATCCGCAGCCTTACACCTTAACTAGCTGCTGCATTATTTTATTTTATTTTATTTTATTTT
GTATTTATTCATCAGGAATAAAAAAACAAGTTTTATTAAAGATTGAAAATTTGATACA
TTTTACAGAACTAATTGTGATGTACATATCAGTGGTGACATATTATTACTTTTTTGGGG
ACGGGGGGTGGGTGGGTGAAGAGATCTTGTGATTTTTTAAGAACCTGCTGGCAAGAGTT
AACTTGTCTTCAGCATATTCTGATTGTATCATAATCATTTTTCTGCTGTTGCAGAGGATGT
GAATACACTTAAGGAGCTCACAGAATCCCAGTAGCACAAATTGGGCTTTGGCAAATCGTG
TATTTTGTGTATAGAAGGAATTTAAGGAGAGGTATTACTTATTTTCATATTGTATTTTAA
CTGTTTCTCTGATCAAATTTTTTTTACTTCCTCCTCCTGTTCTCCTCCACCTCCCTCCTT
TCCAGTTCAGTATTTGGAGTTCAACACTGTCTCTCAATCAGATCATCTTGATCTTTTTCT
TTATCTCCCTTCCCTTCTTAAGTCCCATTTCTTGGTCATAAATATTGCATTATTCACAC
TTTCAAACCTGTGTATTTTCTTACAATAAAAAATGATGAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 20 SULU3 HUMAN

TATTGAATTGGCGGAACGGAAGCCTCCTTTATTTAATATGAATGCAATGAGTGCCTTATA
TCACATAGCCCAAATGAATCCCCTACACTACAGTCTAATGAATGGTCTGATTATTTTCG
CAACTTTGTAGATTCTTGCCTCCAGAAAATCCCTCAAGATCGACCTACATCAGAGGAACT
TTTAAAGCACATATTTGTTCTTCGGGAGCGCCCTGAAACCGTGTTAATAGATCTCATTCA
GAGGACAAAGGATGCAGTAAGAGAGCTGGACAATCTGCAGTATCGAAAGATGAAGAACT
CCTTTTCCAGGAGGCACATAATGGACCAGCAGTAGAAGCACAGGAAGAAGAAGAGGAACA
AGATCATGGTGTTGGCCGGACAGGAACAGTTAATAGTGTTGGAAGTAATCAATCCATTCC
CAGCATGTCCATCAGTGCCAGCAGCCAAAGCAGTAGTGTTAACAGTCTTCCAGATGTCTC
AGATGACAAGAGTGAGCTAGACATGATGGAGGGAGACCACACAGTGATGTCTAACAGTTC
TGTTATCCATTTAAAACAGAGGAAGAAAATTACAGAGAAGAGGGAGATCCTAGAACAAAG
AGCATCAGATCCACAATCTCCACCCCAAGTATCTCGTCACAAATCACACTATCGTAATCG
AGAACACTTTTGCTACTATACGGACAGCATCACTGGTTACGAGGGCAAATGCAAGAACATGA
GCAGGACTCTGAGCTTAGAGAACAAATGTCTGGCTATAAGCGAATGAGGCGACAACATCA
AAAGCAACTGATGACTCTGGAAAACAAGCTAAAGGCTGAGATGGATGAACATCGCCTCAG
ATTAGACAAAGATCTTGAAACTCAGCGTAACAATTTTGCTGCAGAAATGGAGAACTTAT
CAAGAAACACCAGGCTGCCATGGAGAAAGAGGCTAAAGTGATGTCCAATGAAGAGAAAAA
ATTTAGCAACATATTCAGGCCCAACAGAAGAAAGAACTGAATAGTTTTCTCGAGTCCCA
GAAAAGAGAGTATAAACTTCGAAAAGAGCAGCTTAAAGAGGAGCTAAATGAAAACCAGAG
TACCCCCAAAAAAGAAAAACAGGAGTGGCTTTCAAAGCAGAAGGAGAATATACAGCATTT
CCAAGCAGAAGAAGAAGCTAACCTTCTTCGACGTCAAAGACAATACCTAGAGCTGGAATG
CCGTCGCTTCAAGAGAAGAATGTTACTTGGGCGTCATAACTTAGAGCAGGACCTTGTCAG
GGAGGAGTTAAACAAAAGACAGACTCAGAAGGACTTAGAGCATGCCATGCTACTCCGACA
GCATGAATCTATGCAAGAACTGGAGTTCGCCACCTCAACACAATTCAGAAGATGCGCTG
TGAGTTGATCAGATTACAGCATCAAACCTGAGCTCACTAACCAGCTGGAATATAATAAGCG
AAGAGAACGAGAACTAAGACGAAAGCATGTCATGGAAGTTCGACAACAGCCTAAGAGTTT

GAAGTCTAAAGAACTCCAAATAAAAAAGCAGTTTTCAGGATACCTGCAAAATCCAAACCAG
ACAGTACAAAGCATTAAGAAATCACCTGCTGGAGACTACACCAAAGAGTGAGCACAAAGC
TGTTCTGAAACGGCTCAAGGAGGAACAGACCCGGAAATTAGCTATCTTGGCTGAGCAGTA
TGATCACAGCATTAAATGAAATGCTCTCCACACAAGCCCTGCGTTTGGATGAAGCACAGGA
AGCAGAGTGCCAGGTTTTGAAGATGCAGCTGCAGCAGGAACTGGAGCTGTTGAATGCGTA
TCAGAGCAAAATCAAGATGCAAGCTGAGGCACAACATGATCGAGAGCTTCGCGAGCTTGA
ACAGAGGGTCTCCCTCCGGAGGGCACTCTTAGAACAAGATTGAAGAAGAGATGTTGGC
TTTGCAGAATGAGCGCACAGAACGAATACGAAGCCTGTTGGAACGTCAAGCCAGAGAGAT
TGAAGCTTTTGA CTCTGAAAGCATGAGACTAGGTTTTAGTAATATGGTCCTTTCTAATCT
CTCCCCTGAGGCATTTCAGCCACAGCTACCCGGGAGCTTCTGGTTGGTCACACAACCCTAC
TGGGGGTCCAGGACCTCACTGGGGTCATCCCATGGGTGGCCACCACAAGCTTGGGGCCA
TCCAATGCAAGGTGGACCCAGCCATGGGGTCACCTTCAGGGCCAATGCAAGGGGTACC
TCGAGGTAGCAGTATGGGAGTCCGCAATAGCCCCAGGCTCTGAGGCGGACAGCTTCTGG
GGGACGGACGGAGCAGGGCATGAGCAGAAGCACGAGTGTCACTTCACAAATATCCAATGG
GTCACACATGTCTTATACATAACTTAATAATTGAGAGTGGCAATTCGCTGGAGCTGTCT
GCCAAAAGAACTGCCTACAGACATCATCACAGCAGCCTCCTCACTTGGGTACTACAGTG
TGGAAAGCTGAGTGCATATGGTATATTTTATTCATTTTTGTAAAGCGTTCTGTTTTGTGT
TACTAATTGGGATGTCATAGTACTTGGCTGCCGGGTTTGTGGTTTGGGGAAATTTTG
AAAAGTGGAGTTGATATTAATAAATAATGTGTATGTGTGTACATATATACACACACAT
ACACATATATTATGCATGTGGTGAAAAGAATTGGCTAGATAGGGGATTTTTCTGAACACT
GCAAAAATAGAACGTAGCAAAATGGCTTCAGTTATCACTTTTGGGTGTCTGTATCCTAAG
AAGTTTCTGAAAAGATCTAAAGCCTTTTTATCCCATATCCCAAATTCTTATGAGCCACTC
ACAGCAGGCAGCATATGTTGAAATAAGTTATTACTGGTACACACCTGCATTGCCTACCA
GTGTATTTATTTGTTATTAAATTGATCTGACTTCTCAGCCTCATTTGGACTAAAAAAGA
AAGCAGAAATCCATGAACACATTGCTTCTCGGCCTTTTGGCTAAGATCAAGTGTAGAAAT
CCATGAACACTAAAGGACTTCATTGATTTTTTCAGAGAGTAGAAAACAACCTTAGTTTTTC
TTTTTTCCTGAATGCGTCATAGGCTTGTGAGTGATTTTTGTCCATTCAATTGTGCCTTCT
TTGTATTATGATAAGATGGGGGTACTTAAGGAGATCACAAGTTGTGTGAGGATTGCATTA
ACAAACCTATGAGCCTTCAATGGGGAAGACCAGAAGGGTGAGAGGGGGCCCTGAAAGTTCA
TATGGTGGGTATGTCCCGCAGCAGAGTGAGGAGATGAAGCTTACGTGTCCTGACGTTTTG
TTGCTTATACTGTGATATCTCATCCTAGCTAAGCTCTATAATGCCCAAGACCCCAACAG
TACTTTTACTTTGTTTGTACAAAAACAAAGACATATAGCCAATACAAATCAAATGCCGGA
GGTGTGTTGATGCCATATTTGCAAATTGCCATCTATTGAAATTCTCGTCACACTACATAGA
CATAATTGTTATCTCCTTTTGGCTTATGTGATTTTTCTGTTTACAAGTAGAATAGCCAATT
ATTTAAATGTTTAGTTGCCACAGTGAACCAGGAGTCACTGAGCCAATGACTTTACCAGCT
GCTGACTAATCTTCATCACCCTGTAGATTTTGCTGCATGTGCAGGTCTCTATTTTTAA
TTGCTGTTTTCTTGCTGCAGTACTTTACAACTTCTAGTTCTGTTGAGACTTAGTGACCA
TTTGGCATCAAGTTAACATCACACAATAGGAAACACCACTTCCACAAGTCTCAAGCCTCA

Fig. 9Q

49/76

GTGCTAAAGTACTACTGAAAAGGAACTAGGAAGTTTGGCCAATT

SEQ ID NO: 21 SULU3 MURINE

GCAGGATGCCATCAACTAACAGAGCAGGCAGTCTAAAGGACCCTGAAATTGCAGAGCTCT
TCTTCAAAGAAGATCCGGAAAAGCTCTTCACAGATCTCAGAGAAATCGGCCATGGGAGCT
TTGGAGCAGTATATTTTGCACGAGATGTGCGTACTAATGAAGTGGTGGCCATCAAGAAAA
TGTCTTATAGTGGAAAGCAGTCTACTGAGAAATGGCAGGATATTATTAAGGAAGTCAAGT
TTCTACAAAGAATAAAACATCCCAACAGTATAGAATACAAAGGCTGCTATTTACGTGAAC
ACACAGCATGGCTTGTAATGGAATATTGTTTAGGATCTGCTTCAGATTTATTAGAAGTTC
ATAAAAAGCCATTACAAGAAGTGGAAATAGCAGCAATTACACATGGTGCTCTCCAGGGAC
TAGCTTATTTACATTCTCATACCATGATCCATAGAGATATCAAAGCAGGAAATATCCTTC
TGACAGAACCAGGCCAAGTGAAACTTGCTGACTTTGGATCTGCTTCCATGGCTTCCCCTG
CCAATTCTTTTGTGGGAACACCATATTGGATGGCCCCAGAAGTAATTTTAGCCATGGATG
AAGGACAGTATGATGGCAAAGTTGATGTATGGTCTCTTGGAATAACGTGTATTGAATTAG
CCGAGAGGAAGCCTCCTTTATTTAATATGAATGCAATGAGTGCCTTATATCACATAGCCC
AAAATGAATCCCCTACACTACAATCTAATATGAATGATTCTTGCCTCCAGAAAATCCCTC
AAGATCGCCCTACATCAGAGGAACTTTTAAAGCACATGTTTGTTCCTTCGAGAGCGCCCTG
AAACAGTGTTAATAGATCTTATTCAAAGGACAAAGGATGCAGTAAGAGAGCTGGACAATC
TGCAGTATCGAAAGATGAAGAAACTCCTTTTCCAGGAGGCACATAATGGGCCAGCGGTAG
AAGCACAGGAAGAAGAGGAGGAGCAAGATCATGGTGTTGGCCGAACAGGAACAGTGAATA
GTGTTGGAAGCAATCAGTCTATCCCTAGTATGTCTATCAGTGCCAGCAGTCAAAGCAGCA
GTGTTAATAGTCTTCCAGATGCATCAGATGACAAGAGTGAGCTAGACATGATGGAGGGAG
ACCATACAGTGATGTCTAACAGTTCTGTCTATCCACTTAAACCTGAGGAGGAAAATTACC
AGGAAGAAGGAGATCCTAGAACAAAGAGCATCAGACCCACAGTCTCCCCCTCAGGTGTCTC
GTCACAAGTCACATTATCGTAATAGAGAACACTTTGCAACCATACGAACAGCATCACTGG
TTACAAGACAGATGCAAGAACATGAGCAGGACTCTGAACTTAGAGAACAGATGTCTGGTT
ATAAGCGGATGAGGCGACAGCATCAAAAGCAGCTGATGACGCTGGAAAATAAACTGAAGG
CAGAGATGGACGAACATCGGCTCAGATTAGACAAAGATCTTGAAACTCAGCGTAACAATT
TCGCTGCAGAAATGGAGAAACTTATTAAGAAACACCAAGCTGCTATGGAAAAAGAGGCTA
AAGTGATGGCCAATGAGGAGAAAAAATTCCAGCAACACATTCAGGCTCAACAGAAAAAAG
AACTGAATAGCTTTTTTGGAGTCTCAAAAAAGAGAATATAAACTTCGCAAAGAGCAGCTTA
AGGAGGAGCTGAATGAAAACAGAGCACACCTAAAAAAGAAAAGCAGGAATGGCTTTCAA
AGCAGAAGGAGAATATACAGCATTTTCAGGCAGAAGAAGAAGCTAATCTTCTTCGACGTC
AAAGGCAGTATCTAGAGCTAGAATGTCGTCGCTTCAAAAGAAGAATGTTACTTGGGCGAC
ATAACTTGGAACAGGACCTTGTCAGGGAGGAGTTAAACAAAAGGCAGACTCAAAAGGACT
TGGAACATGCAATGCTATTGCGACAGCATGAATCAATGCAAGAACTGGAGTTTTCGCCATC
TCAACACTATTGAGAAGATGCGCTGTGAGTTGATCAGACTGCAGCATCAAAGTGAAGCTCA
CTAACCAGCTAGAGTACAATAAGAGAAGGGAACGGGAAGTGAAGGCGAAAACATGTCATGG

Fig. 9R

50/76

AAGTTCGACAACAACCTAAGAGTCTGAAGTCTAAAGAACTCCAAATAAAAAAGCAGTTTC
AGGATACCTGCAAAATTCAAAACCAGACAGTACAAAGCATTAAGGAATCACCTACTGGAGA
CTACACCAAAGAATGAGCACAAAGCAATC

SEQ ID NO: 25 GEK2 HUMAN

CGAAGCCACAGCCCGAGCCCGAGCCCGAGCCCGAGCCGGCGCCACCGCGCCCCCGGCCAT
GGCTTTTGGCAATTTCCGCCGCATCCTGCGCCTGTCTACCTTCGAGAAGAGAAAAGTCCCG
CGAATATGAGCACGTCCGCCGCGACCTGGACCCCAACGAGGTGTGGGAGATCGTGGGCGA
GCTGGGCGACGGCGCCTTCGGCAAGGTTTACAAGGCCAAGAATAAGGAGACGGGTGCTTT
GGCTGCGGCCAAAGTCATTGAAACCAAGAGTGAGGAGGAGCTGGAGGACTACATCGTGGA
GATTGAGATCCTGGCCACCTGCGACCACCCCTACATTGTGAAGCTCCTGGGAGCCTACTA
TCACGACGGGAAGCTGTGGATCATGATTGAGTTCTGTCCAGGGGGAGCCGTGGACGCCAT
CATGCTGGAGCTGGACAGAGGCCTCACGGAGCCCCAGATACAGGTGGTTTGCCGCCAGAT
GCTAGAAGCCCTCAACTTCCTGCACAGCAAGAGGATCATCCACCGAGATCTGAAAGCTGG
CAACGTGCTGATGACCCTCGAGGGAGACATCAGGCTGGCTGACTTTGGTGTGTCTGCCAA
GAATCTGAAGACTCTACAGAAACGAGATTCTTTCATCGGCACGCCTTACTGGATGGCCCC
CGAGGTGGTCATGTGTGAGACCATGAAAGACACGCCCTACGACTACAAAGCCGACATCTG
GTCCCTGGGCATCACGCTGATTGAGATGGCCAGATCGAGCCGCCACACCACGAGCTCAA
CCCCATGCGGGTCCTGCTAAAGATCGCCAAGTCGGACCCTCCCACGCTGCTCACGCCCTC
CAAGTGGTCTGTAGAGTTCCGTGACTTCCTGAAGATAGCCCTGGATAAGAACCCAGAAAC
CCGACCCAGTGCCGCGCAGCTGCTGGAGCATCCCTTCGTCAGCAGCATCACCAGTAACAA
GGCTCTGCGGGAGCTGGTGGCTGAGGCCAAGGCCGAGGTGATGGAAGAGATCGAAGACGG
CCGGGATGAGGGGGGAAGAGGAGGACGCCGTGGATGCCGCCCTCCACCCTGGAGAACCATAC
TCAGAACTCCTCTGAGGTGAGTCCGCCAAGCCTCAATGCTGACAAGCCTCTCGAGGAGTC
ACCTTCCACCCCGCTGGCACCCAGCCAGTCTCAGGACAGTGTGAATGAGCCCTGCAGCCA
GCCCTCTGGGGACAGATCCCTCCAAACCACCAGTCCCCCAGTCGTGGCCCCTGGAAATGA
GAACGGCCTGGCAGTGCCCTGTGCCCCTGCGGAAGTCCCGACCCGTGTCAATGGATGCCAG
AATTCAGGTAGCCCAGGAGAAGCAAGTTGCTGAGCAGGGTGGGGACCTCAGCCCAGCAGC
CAACAGATCTCAAAAGGCCAGCCAGAGCCGGCCCAACAGCAGCGCCCTGGAGACCTTGGG
TGGGGAGAAGCTGGCCAATGGCAGCCTGGAGCCACCTGCCCAGGCAGCTCCAGGGCCTTC
CAAGAGGGACTCGGACTGCAGCAGCCTCTGCACCTCTGAGAGCATGGACTATGGTACCAA
TCTCTCCACTGACCTGTCGCTGAACAAAGAGATGGGCTCTCTGTCCATCAAGGACCCGAA
ACTGTACAAAAAACCTCAAGCGGACACGCAAATTTGTGGTGGATGGTGTGGAGGTGAG
CATCACCACTCCAAGATCATCAGCGAAGATGAGAAGAAGGATGAGGAGATGAGATTTCT
CAGGCGCCAGGAACTCCGAGAGCTTCGGCTGCTCCAGAAAGAAGAGCATCGGAACCAGAC
CCAGCTGAGTAACAAGCATGAGCTGCAGCTGGAGCAAATGCATAAACGTTTTGAACAGGA
AATCAACGCCAAGAAGAAGTTCTTTGACACGGAATTAGAGAACCTGGAGCGTCAGCAAAA
GCAGCAAGTGGAGAAGATGGAGCAAGACCATGCCGTGCGCCGCCGGGAGGAGGCCAGGCG

Fig. 9S
51/76

GATCCGCCTGGAGCAGGATCGGGACTACACCAGGTTCCAAGAGCAGCTCAAACCTGATGAA
GAAAGAGGTGAAGAACGAGGTGGAGAAGCTCCCCGACAGCAGCGGAAGGAAAGCATGAA
GCAGAAGATGGAGGAGCACACGCAGAAAAAGCAGCTTCTTGACCGGGACTTTGTAGCCAA
GCAGAAGGAGGACCTGGAGCTGGCCATGAAGAGGCTCACCCACCGACAACAGGCGGGAGAT
CTGTGACAAGGAGCGCGAGTGCCTCATGAAGAAGCAGGAGCTCCTTCGAGACCGGGAAGC
AGCCCTGTGGGAGATGGAAGAGCACCAGCTGCAGGAGAGGCAACCAGCTGGTGAAGCAGCA
GCTCAAAGACCAGTACTTCCTCCAGCGGCACGAGCTGCTGCGCAAGCATGAGAAGGAGCG
GGAGCAGATGCAGCGCTACAACCAGCGCATGATAGAGCAGCTGAAGGTGCGGCAGCAACA
GGAAAAGGCGCGGCTGCCCAAGATCCAGAGGAGTGAGGGCAAGACGCGCATGGCCATGTA
CAAGAAGAGCCTCCACATCAACGGCGGGGGCAGCGCAGCTGAGCAGCGTGAGAAGATCAA
GCAGTTCTCCCAGCAGGAGGAGAAGAGGCAGAAGTCGGAGCGGCTGCAGCAACAGCAGAA
ACACGAGAACCAGATGCGGGACATGCTGGCGCAGTGCGAGAGCAACATGAGCGAGCTGCA
GCAGCTGCAGAATGAAAAGTGCCACCTCCTGGTAGAGCACGAAACCCAGAAACTGAAGGC
CCTGGATGAGAGCCATAACCAGAACCTGAAGGAAT

SEQ ID NO: 27 PAK4 HUMAN

CGTTCCTGGGCTTCCCGCTCCGCAGGCCTGCGGAGGACTGGCCCAGCAAGGTCCCAGGTC
TTCCCTCTCCTTAGCGCCTAAGAGAGAGGGCCAGTGCGGGTGAGGAGTCGCGAGGAAGAG
GCGGAAGGCGCCGGAAGGCACCATGTTCCGCAAGAAAAAGAAGAAACGCCCTGAGATCTC
AGCGCCACAGAACTTCCAGCACCGTGTCCACACCTCCTTCGACCCCAAGAAGGCAAGTT
TGTGGGCCTCCCCCACAATGGCAGAACATCCTGGACACACTGCGGCGCCCCAAGCCCGT
GGTGGACCCTTCGCGAATCACACGGGTGCAGCTCCAGCCCATGAAGACAGTGGTGCGGGG
CAGCGCGATGCCTGTGGATGGCTACATCTCGGGGCTGCTCAACGACATCCAGAAGTTGTC
AGTCATCAGCTCCAACACCCTGCGTGGCCGCAGCCCCACCAGCCGGCGGGGCACAGTC
CCTGGGGCTGCTGGGGGATGAGCACTGGGCCACCGACCCAGACATGTACCTCCAGAGCCC
CCAGTCTGAGCGCACTGACCCCCACGGCCTCTACCTCAGCTGCAACGGGGGCACACCAGC
AGGCCACAAGCAGATGCCGTGGCCCGAGCCACAGAGCCCACGGGTCTGCCCAATGGGCT
GGCTGCAAAGGCACAGTCCCTGGGCCCCGCGAGTTTCAGGGTGCTCGCAGCGCTGTCT
GCAGCTGGGTGCCTGCCTGCAGAGCTCCCCACCAGGAGCCTCGCCCCCACGGGCACCAA
TAGGCATGGAATGAAGGCTGCCAAGCATGGCTCTGAGGAGGCCCGGCCACAGTCCTGCCT
GGTGGGCTCAGCCACAGGCAGGCCAGGTGGGGAAGGCAGCCCTAGCCCTAAGACCCGGGA
GAGCAGCCTGAAGCGCAGGCTATTCCGAAGCATGTTCTGTCCACTGCTGCCACAGCCCC
TCCAAGCAGCAGCAAGCCAGGCCCTCCACCACAGAGCAAGCCCAACTCCTCTTTCCGACC
GCCGCAGAAAGACAACCCCCCAAGCCTGGTGGCCAAGGCCCAGTCCTTGCCCTCGGACCA
GCCGGTGGGGACCTTCAGCCCTCTGACCACTTCGGATAACAGCAGCCCCCAGAAGTCCCT
CCGCACAGCCCCGGCCACAGGCCAGCTTCCAGGCCGGTCTTCCCCAGCGGGATCCCCCG
CACCTGGCACGCCCAGATCAGCACCAAGCAACCTGTACCTGCCCCAGGACCCCCACGGTTGC
CAAGGGTGCCCTGGCTGGTGAAGGACACAGGTGTTGTGACACATGAGCAGTTCAAGGCTGC

Fig. 9T
52/76

GCTCAGGATGGTGGTGGACCAAGGGTGACCCCCGGCTGCTGCTGGACAGCTACGTGAAGAT
TGGCGAGGGGCTCCACCGGCATCGTCTGCTTGGCCCCGGGAGAAGCACTCGGGCCGCCAGGT
GGCCGTCAAGATGATGGACCTCAGGAAGCAGCAGCGCAGGGAGCTGCTCTTCAACGAGGT
GGTGATCATGCGGGACTACCAGCACTTCAACGTGGTGGAGATGTACAAGAGCTACCTGGT
GGGCGAGGAGCTGTGGGTGCTCATGGAGTTCCTGCAGGGAGGAGCCCTCACAGACATCGT
CTCCCAAGTCAGGCTGAATGAGGAGCAGATTGCCACTGTGTGTGAGGCTGTGCTGCAGGC
CCTGGCCTACCTGCATGCTCAGGGTGTCTCCACCGGGACATCAAGAGTGACTCCATCCT
GCTGACCCTCGATGGCAGGGTGAAGCTCTCGGACTTCGGATTCTGTGCTCAGATCAGCAA
AGACGTCCCTAAGAGGAAGTCCCTGGTGGGAACCCCCCTACTGGATGGCTCCTGAAGTGAT
CTCCAGGTCTTTGTATGCCACTGAGGTGGATATCTGGTCTCTGGGCATCATGGTGATTGA
GATGGTAGATGGGGAGCCACCGTACTTCAGTGACTCCCCAGTGCAAGCCATGAAGAGGCT
CCGGGACAGCCCCCACCCAAGCTGAAAACTCTCACAAGGTCTCCCCAGTGCTGCGAGA
CTTCCTGGAGCGGATGCTGGTGCGGGACCCCCAAGAGAGAGCCACAGCCCAGGAGCTCCT
AGACCACCCCTTCCTGCTGCAGACAGGGCTACCTGAGTGCCCTGGTGCCCTGATCCAGCT
CTACCGAAAGCAGACCTCCACCTGCTGAGCCCCACCCCAAGTATGCCTGCCACCTACGCCC
ACAGGCAGGGCACACTGGGCAGCCAGCCTGCCGGCAGGACTTGCCCTGCCTCCTCCTCTCA
GTATTCTCTCCAAAGATTGAAATGTGAAGCCCCAGCCCCACCCTCTGCCCTTCAGCCTAC
TGGGCCAGGCCGGACCTGCCCCCTCAGTGTCTCTCCCTCCCGAGTCCCCAGATGGAGACC
CCTTTCTACAGGATGACCCCTTGATATTTGCACAGGGATATTTCTAAGAAACGCAGAGGC
CAGCGTTCCTGGCCTCTGCAGCCAACACAGTAGAAAAGGCTGCTGTGGTTTTTTTAAAGGC
AGTTGTCCACTAGTGTCCTAGGCCACTGCAGAGGGGCAGACTGCTGGTCTCCACAGATACC
TGCTGTTCTCAGCTCCAGCTTCAAACCTCGAGTCTCGAGAGGGCCACGGGGTGGTTTTTA
TGACCGGAATCCCGCTTCCTCCCTCACGTCTGATGTCCTGAAGGTGCAGTCCCACCTGTA
CAGCCCCCTCCCCGCCAAGAACTGTGAATGGCCTGCTCCAGGCCATGGCTGGGGGCAGGGA
GTGAGGGGACAATTTCTGAGTGAAAGAGAAAGAATGGGGTCGGTGGTGAAGGTGCTCTCA
CTTTACAGAATGGAGAGAACATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TG
CCTCCAGGTACCCACAGCCAGTTTCAGGAAGGCTGCCCCCTCTCTCCCACTAAGTTCTGG
CCTGAAGGGACCTGCTTTCTTGGCCTGGCTTCCACCTCTCCACTCCTGTGTCTACCTGGC
CAGTGGAGTGGTCCATGCTAAGTCTAACACTCCTGGGAGCTCAGGAGGCTTCTGAGCTTC
TCCTGTACTGTGCATCGTGAGGGCCAGAGACAGGAATGTAAGGATTGGCAACTGTGTTAC
CTTTCAAGTTTATCTCAATAACCAGGTCATCAGGGACCCATTGTTCTCTTCAGAACCTTA
TCTGGGAGAGAAGGCGAACCACCTCCGGGTTTCCATCATGTCAAGGTCACAGGCATCCAT
GTGTGCAAACCATCTGCCCCAGCTGCCTCCACAGACTGCTGTCTCCTTGTCTCCTCGGC
CCTGCCCCACTTCAGGGCTGCTGTGAGATGGAATTCCAGGAAAGAACTTCAGGTGTCTGG
ACCCTTTCTATCTAGATAATATTTTTTAGATTCTTCTGCTCCCTAGTGACCTACCTGGGGG
CAAAGAAATTGCAAGGACTTTTTTTTTAAGGGTCAGAGTTTTTCAAAACAAAAGCATCTTCC
CTAGAAATTTTTGTGAATTGTTTGCACCTTGTGCCTGTTTTAAATTAAATTGAGTGTTCAA

Fig. 9U

AGCC

SEQ ID NO: 28 PAK5 HUMAN

GGCCAGTGGGGCGAAACTGGCAGCTGGCCGGCCCTTTAACACCTACCCGAGGGCTGACAC
GGACCACCCATCCCGGGGTGCCCAGGGGGAGCCTCATGACGTGGCCCTAACGGGGCCATC
AGCGGGGGGCTGGCCATCCCCCAGTCCTCCTCCTCCTCCTCCCGGCCTCCCACCCGAGC
CCGAGGTGCCCCCAGCCCTGGAGTGCTGGGACCCCCACGCCTCAGAGCCCCAGCTGGCCCC
TCCAGCCTGCACCCCCGCCGCCCTGCTGTTCTTGGGCCCCCTGGCCCCCGCTCACCACA
GCGGGAGCCACAGCGAGTATCCCATGAGCAGTTCCGGGGCTGCCCTGCAGCTGGTGGTGGA
CCCAGGCGACCCCCGCTCCTACCTGGACAACCTTCATCAAGATTGGCGAGGGCTCCACGGG
CATCGTGTGCATCGCCACCGTGCGCAGCTCGGGCAAGCTGGTGGCCGTCAAGAAGATGGA
CCTGCGCAAGCAGCAGAGGCGCGAGCTGCTCTTCAACGAGGTGGTAATCATGAGGGACTA
CCAGCACGAGAATGTGGTGGAGATGTACAACAGCTACCTGGTGGGGGACGAGCTCTGGGT
GGTCATGGAGTTCCTGGAAGGAGGCGCCCTCACCGACATCGTCACCCACACCAGGATGAA
CGAGGAGCAGATCGCGGCCGTGTGCCTTGCAGTGCTGCAGGCCCTGTCGGTGCTCCACGC
CCAGGGCGTCATCCACCGGGACATCAAGAGCGACTCGATCCTGCTGACCCATGATGGCAG
GGTGAAGCTGTCAGACTTTGGGTTCTGCGCCCAGGTGAGCAAGGAAGTGCCCCGAAGGAA
GTCGCTGGTCGGCACGCCCTACTGGATGGCCCCAGAGCTCATCTCCCGCCTTCCCTACGG
GCCAGAGGTAGACATCTGGTCGCTGGGGATAATGGTGATTGAGATGGTGGACGGAGAGCC
CCCCTACTTCAACGAGCCACCCCTCAAAGCCATGAAGATGATTCGGGACAACCTGCCACC
CCGACTGAAGAACCTGCACAAGGTGTCGCCATCCCTGAAGGGCTTCTTGGACCGCCTGCT
GGTGCGAGACCCTGCCCAGCGGGCCACGGCAGCCGAGCTGCTGAAGCACCCATTCTGGC
CAAGGCAGGGCCGCCTGCCAGCATCGTGCCCTCATGCGCCAGAACCGCACCCAGATGAGG
CCCAGCGCCCTTCCCCTCAACCAAAGAGCCCCCCCCGGGTACCCCCGCCCACTGAGGCC
AGTAGGGGGCCAGGCCTCCCCTCCTCCAGCCCCGGGAGATGCTCCGCGTGGCACCCACC
TCCTTGCTGGGGGTAGATGAGACCCTACTACTGAACTCCAGTTTTGATCTCGTGACTTTT
AGAAAAACACAGGGACTCGTGGGAGCAAGCGAGGCTCCCAGGACCCCCACCTCTGGGAC
AGGCCCTCCCCCATGTTCTTCTGTCTCCAGGAAGGGCAGCGGCCCTCCCATCACTGGAAG
TCTGCAGTGGGGGTGCTGGGGGTGGAGAGAACTAAGAGGTGAACATGTATGAGTGTG
TGCACGCGTGTGAGTGTGCATGTGTGTGTGTGTGCAAAGGTCCAGCCACCCCGTCCTCCA
GCCCGCAAGGGGTGTCTGGCGCCTTGCTGACACCCAGCCCCCTCTCCCCCTGAGCCATT
GTGGGGGTGATCATGAATGTCCGAAGAGTGGCCTTTTCCCGTAGCCCTGCGCCCCCTTT
CTGTGGCTGGATGGGGAGACAGGTCAGGGCCCCCACCCTCTCCAGCCCCCTGCAGCAAAT
GACTACTGCACCTGGACAGCCTCCTCTTTTCTAGAAGTCTATTTATATTGTCATTTTATA
ACACTCTAGCCCCCTGCCCTTATTGGGGGACAGATGGTCCCTGTCTGCGGGGTGGCCCTG
GCAGAACCACTGCCTGAAGAACCAGGTTCTTGCCCGGTGAGCGCAGCCCCAGCCCGCCCA
CCCCTGCCTCGAGTTAGTTTTACAATTAACATTGTCTTGTGTTTTGTGAAAAAAAAAAAA
AAAAAAAAAA

Fig. 9V
54/76

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MSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEMVTLQGELHVSKLFNHPNIVPYRATFI
ADNELWVTSFMAYGSAKDLICTHFMDSGMNELAIAYILQVLKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRSNL
SMISHGQRQVRVHDFPKYSVKVLPWLSPEVLQQLQGYDAKSDIYSVGITACELANGHVPFKDPATQMLLEKLNGLTVPC
LLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPSHPHYHRTFSPHFHFVEQCLQRNPDARPSASTLLNHSF
FKQIKRRASEALPELLRPVPTITNFEQSQDHSIGIFGLVTNLEELEVDWDF

>STLK6_h

MSLLDCFCSTRTQVESLRPEKQSETSIHQYLVDEPTLSWSRPSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHT
PTGTLVTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVFTVGSWLWVISPFMAYGSASQLLRTYFPEGMSETL
IRNILFAGVRLNYLHQNCIHRSIKASHILISGDGLVTLGSLSHLSLVKHGQRHRAVYDFPQFSTSVQPWLSPELLRQ
DLHGYNVKS DIYSVGITACELASGVVPFQDMHRTQMLLQKLKPPYSPLDISIFPQSESRMKNSSQSGVDSGIGESVLVSS
GHTVNSDRLHTPSSKTFSPAFFSLVQLCLQQDPEKRPSASSLLSHVFFKQMKESQDSILSLLPPAYNKPSISLPPVLP
WTEPECDFPDEKDSYWEF

51
55/76

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NRDDYELQEVIGSGATAVVQAA YCAPKKEKVAIKRINLEKQCQTSMDPELLKEIQAMSQCHHPNIVSYTTSFVVKDELWLVM
KLSSGGSVLDIKIHIVAKGEHKS

>ZC4_h

MAGPGGWRDREVTDLGHLDPDTGIFSLDKTIGLTGYGRIYLG LHEKTGAFTAVKVMNARKDEEEDLRTELNLLRKYSFHK
NIVSYGAFKLSPPGQRHQLWMVMELCAAGSVTDVVRMTSNQSLKEDWIA YICREILQGLAHLHAHRV IHRDIKGNVL
LTHNAEVKLVD FGVSAQVSR TNGRRNSFIGTPYWM APEVIDCEDPRRSYDYRSDVSWSGITAIEMAEGAPPLCNLQPLE
ALFVILRESAPT V KSSGWSRK FHNFM EKCTIKN FLFRPT SANMLQHPFVRDIKNERHVVESLTRH LTGIIKKRQKKEQAR
EKKS K VSTLRQALAKRLSPKRFRAKSSWRPEKLELSDLEARRQRRR WEDIFNQHEEELRQVDKDEESSDNDEVFHS

Fig. 10A

IQA EVQIE PLKPYISNP K KIEVQERSPSVPNNQDHAHV K FSSV PQRSLLEQA QKPIDIRQRSSQNRQNWLAASGDSKH
KILAGKTQSYCLTIYISEVKKEEFQEGMNQKCQGAQVGLGPEGHC IWQLGESSSEEEESPVTGRRSQSSPPYSTIDQKLLV
DIHVPDGFVKISPPVYLTNEWVGYNALSEIFRNDWLTAPV IQPPEEDGDYVELYDASADTDGDDDDDESNDTFEDTYD
HANGNDDLDNQVDQANDVC KDHDDNNKFVDDVNNNYEAPSCPRASYGRDGSCKQDGYDGSRGKEEAYRGYGSHTANRS
HGGSAASEDNAAIGDQEEHAANIGSERRGSEGDGKG VVRTSEESGALGLNGEENCSETDGPGLKRPASQDFFEYLQEEPG
GGNEASNAIDGAAPSAPDHESDNKDISESTQSDFSANHSSPSKSGMSADANFASAILYAGFVEVPEESPQKQPSSEVNV
NPLYVSPACKKPLIHM YEKEFTSEICCGSLWGVNLLGTRSNLYLMDRSGKADITKLIRRRPFRQIQVLEPLNLLITISG
HKNRLRVYHLTWLRNKILNNDPESKR RQEEMLKTEEACKAIDKLTGCEHFSVLQHEETTYIAIALKSSIHLYAWAPK'SFD
ESTA IKVFPTLDHKPVTVDLAIGSEKRLKIFFSSADGYHLIDA ESEVMSDVTLPKNPLEIIIPQNIILPDCLGIGMMLT
FNAEALSVEANEQLFKKILEMWK DIPSSIAFECTQRTTGWGQK AIEVRSLSQSRVLESELKRRS IKKLRFLCTRGD KLFFT
STLRNHHSRVYFMTLGKLEELQSNYDV

56/76

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MFGKRKRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWQSLIEESARRPKPLVDPACITSIQPGAPKTIVRGSKGAKDG
ALTLLDEFENMSVTRSNLSRRDSPPPPARARQENGMP EEPATTARGGPGKAGSRGRFAGHSEAGGGSGDRRRRAGPEKRP
KSSREGSGGPQESSRDKRPLSGPDVGTQPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAPNGPSAGGLAIP
QSSSSSRPPTRARGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQREPQRVSH EQFRAALQLVVDPGDPRSY
LDNFIKIGEGSTGIVCIATVRSSGKLVA VKKMDLRKQQRRELLFNEVIMRDYQHENVVEMYN SYLVGDELWVVMFELEG
GALTDIVTHTRMNEEQIAAVCLAVLQALSVLHAQGV IHRDIKSDSILLTHDGRVKLSDFGCAQVSKEVPRRKSLVGTPY
WMAPELISRLPYGPEVDIWSL GIMVIEMVDGEPYPYFNEPPLKAMKMIRDNLPPRLKNLHKVSPSLKGFLDRLLVRDPAQR
ATAAELLKHPFLAKAGPPASIVPLMRQNRT

>GEK2_h

MAFANFRRIILRLSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVYKAKNKETGALAAAKVIETKSEEELEDYIV
EIEILATCDHPYIVKLLGAYYHDGKLIWIMIEFCPGGAVDAIMLELD RGLTEPQIQVVC RQMLEALNFLHSKR IIRDLKA

Fig. 10B

GNVLMTEGDIRLADFGVSAKNLKTLLQKRDSFIGTPYWMapevVMCETmKdTPYdYKADIWSLgITLIEMaQIEPPHHEL
NPMRVLLKIAKSDPPTLLTPSKWSVEFRDfLKIALDKNPETRPSAAQLLEHPFVSSITSNKALRELVAEAKAEVMEEIED
GRDEGEEDAVDAASTLENHTQNSSEVSPPSLNADKPLEESPSTPLAPSQSDSVNEPCSPSGDRSLQTTSPPVVAPGN
ENGLAVPVPLRKSRPVSMDARIQVAQEKQVAEQGGDLSPAANRSQKASQSRPNSSALETLGGEKLANGSLEPPAQAAAPGP
SKRSDCSSLCTSESMDYGTNLSTDLSLNKEMGSLSIKDPKLYKKTLLKTRKFVVDGVEVSIITTSKIISEDEKKDEEMRF
LRRQELRELRLLLQKEEHRNQTL SNKHHELQLEQMhKRFEQEI NAkkFFDTELEnLERQQKQKQVEKMEQDHAVRRREEAR
RIRLEQDRDYTRFQEQ LKMKKEVKNEVEKLPRQQRKESMKQKMEEHtQKKQLLDRDFVAKQKEDLELAmKRLTTDNRRRE
ICDKEREC LMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHELLRKHEKEREQMQRYNQRMIEQLKVRQQ
QEKARLPKIQRSEGKTRMAMYKKS LHINGGSAAEQREKIKQFSQQEEKRQKSERLQQQKHENQM RDMLAQCESNMSEL
QQLQNEKCHLLVEHETQKLKALDESHNQNLKEWRDKL RPRKKALEEDLNQKKREQEMFFKLSEEAECNPSTPSKAAKFF
PYSSGDAS

Fig. 10C

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GGCCAAAGACGGTCGGGGCTGCTTAACTCCAGGAACAGGTTTAAAGTTTTTGAACCTGAAGTAGGTTCTACACAGTAGGA
ACTCATGTCTATTTCTTAAGTAAACAGAGCGAATCAGCGGTCTCGGAAAGTTTCATTGTTGAGGGCTTAAAGAG
ATTTGGAACCTATTTGGAGACCAATGATGCGAGCTCAGAGTCAATAGCATCCTTCTCTAAACAGGAGTTCATGAGTAGCTT
TCTGCCAGAGGGAGGTGTTACGAGCTGCTCAGTGTGATAGGCAAAAGGATTTGAGGACCTGTGATGACTGTGAATCTAGCAA
GGTACAAACCAACAGGAGAGTACGTGACTGTACGGAGGATTAAACCTAGAAAGCTTGTCCAAATGAGATGGTAACATTCTTG
CAGGGCGAGCTGCATGCTCCAAACTTCAACCATCCCAATATCGTGCCATATCGAGGCCACTTTTATTGCAGACAATGA
GCTGTGGGTTGTACATCATTTGTCATGGCATACGGTTCTGCAAAAGATCTCATCTGTACACACTTCATGGATGGCATGAATG
AGCTGGCGATTGCTTACATCTGCAGGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGT
GTCAAAAGCCAGCCACATCCTGATCTCTGTGGATGGGAAGTCTACCTGTCTGGTTTGGCGAGCAACCTCAGCATGATAAG
CCATGGGCGAGCGGAGGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGTTCTGCCGTGGCTCAGCCCCGAGGTCC
TCCAGCAGAATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACCTGGCCAAACGGC
CATGTCCCCCTTTAAGGATATGCTTGCACCCAGATGCTGTAGAGAACTGAACGGCACAGTGGCCCTGCTGCTGTTGGATAC
CAGCACCATCCCCGCTGAGGAGCTGACCATGAGCCCCCTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACAGCCTGACCA
CCAGCACCCCCGGCCCTCCAAACGGTGACTCGCCCTCCACCCCTACCCAGCAACCTTCTCCCCCACTTCCACCACTTT
GTGGAGCAGTGCCCTCAGCGCAACCCGGATGCCAGGCCAGTGCCAGCACCTCCTGAACCACTCTTCTTCAAGCAGAT
CAAGCGACGTGCTCAGAGGCTTTGCCCGAATTGCTTCGTCTGTACCCCCCATCACCAATTTTGAGGGCGAGCCAGTCTC
AGGACCACAGTGGAACTTTTGGCCCTGGTAACAAACCTGGAAGAGCTGGAGGTGGACGATTGGGAGTTCTGAGCCCTCTGCA
AACTGTGCGCATTTCCAGCCAGGATGCGAGGCCACCCAGAGGCCCTTCTCTGAGGGCCGGCCACATTCCTCCGCCCTCCT
GGGCAGATTGGGTAGAAAGGACATTTCTCCAGGAAAGTTGACTGCTGACTGATTGGGAAGAAATCCTGGAGAGATACT
TCACTGCTCCAAGGCTTTTGAGACACAAAGGGAATCTCAACACAGGATCAGGAGGTCCAAAGCCGACATTCCTCAGTC
CTGTGAGCTCAGGTGACCTCTCCGCGAAGAGAGATGCTGCTCTGGCCCTGGGAGCTGAATTCGAAGCCAGGGTTTGG
CTCCTTAAACCCGAGGACCGCCACCTCTTCCAGTGCTTGGCAGCCAGCTCATTTCTATTAACTTTGCTCTCAGATGCTT
CAGATGCTATAGGTGAGTGAAGGGCAAGTAGTAAGCTGCCCTCCCTTCCCTCAGACCTCTCCCTCATAAATCCAGA
GAAGGGCATTTCTGCTTTTAAAGCACAGACTAAGGCTGGAAACAGTCCATCTTATCCCTCTTCTGGCTTGGGCCCTGAC

58/76

Fig. 11A

ACCTAAGTCTTTCCACGGTTTATGTGTGCCCTCATTCCTTTCCACCAAGAAATCCATCTTAGCGCCTCCTGCCAGCTG
CCCTGGTGCTTTCTCCAGGGCCATCAGTGTCTTTGCCTAGCTTGAGGGCTTAAGTCCTTATGCTGTGTTAGTTTCGTTGT
CAGAACAAATTAAATTTTCAGAGACGCTG

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AAGGAAGATAAAACAAAGCCTTCTTTGGAAATAGATGGATTTTGTCACTTTCTGTGAACTAAAGTGATTCAATGTCT
CTTTGGATTGCTTCTGCACCTTCAAGAACACAAAGTTGAATCACTCAGACCTGAAAAACAGTCTGAAACCCAGTATCCATCA
ATACITGGTIGATGAGCCAAACCCCTTTCTGCTCACGTCACCTCCACTAGAGCCAGTGAAGTACTATGTTCACCCAAACGTTT
CTCACTATGAGCTCCAAGTAGAAATAGGAAGAGGATTTGACAACTTGACITCTGTCCATCTTGACCGGCATACTCCACG
GGAACACTGGTAACATAAAATTAACAAATCTGGAAACTGCAATGAAGAACGCCCTGAAAGCTTTACAGAAAGCCGTGAT
TCTATCCCACTTTTCCGGCATCCCAATATTACAACTTATTGGACAGTTTTCACGTGTGGCAGCTGGCTTTGGGTTATTT
CTCCATTTATGGCCATATGGTTCAGCAAGTCAACTCTTGAGGACCTATTTTCTGAAGGAATGAGTGAACTTTAATAAGA
AACATTCTCTTTGGAGCCGTGAGGGTTGAACATATCTGCACCAAAATGGCTGTATTCACAGGAGTATTAAAGCCAGCCA
TATCCTCATTTCTGGTATGGCCTAGTGACCCCTCTCTGGCCCTTCCCATCTGCATAGTTTGTTAAGCATGGACAGAGGC
ATAGGGCTGTGTATGATTTCCACAGTTCAGCACATCAGTGCAGCCGTGGCTGAGTCCAGAACTACTGAGACAGGATTTA
CATGGGTATAATGTGAAGTCAGATATTTACAGTGTGGGATTACAGCATGTGAATTAGCCAGTGGGCAGGTGCCTTTCCA
GGACATGCATAGAACTCAGATGCTGTTACAGAAACTGAAAGGTCTCTCTTATAGCCCATTTGGATATCAGTATTTTCCCTC
AATCAGAAATCCAGAAATGAAAAATTTCCAGTCAGGTGTAGACTCTGGGATTGGAGAAAGTGTGCTTGTCTCCAGTGGAACT
CACACAGTAAATAGTGACCGATTACACACACCATCTCTCAAAACTTCTCTCTGCTTCTTAGCTTGGTACAGCTCTG
TTTGCAACAAGATCCTGAGAAAGGCCATCAGCAAGCAGTTTATTGTCCCATGTTTCTTCAACAGATGAAAGAAAGAA
GCCAGGATTCAATACTTTCACTGTGCTCTCTGCTTATAACAAGCCATCAATATCATTTGCCCTCCAGTGTACCTTGGACT
GAGCCAGAAATGTGATTTTCCCTGATGAAAAAGACTCATACTGGGAATTTCTAGGGCTGCCAAATCATTTTATGTCTATATA
CTTGACACTTTCTCTGTGCTTTTCTCTGTATTTCTAGGTACAAATACCAGAAATTATACCTTGAAATACAGTTGGT
GCACITGGAGAAATCTATTATTAAACCACTCTGTTCAAAGGGGCACCAAGTTGTAGTCCCTCTGTTCGACACAGTACT
ATGACAAGGAACATCAGAAATTAATACTAGCTAGTGTCAATTTATCTGGAAATTTTCTAAGCTGTGACTAATCTT

59/76

Fig. 11B

TTTATCTCAATAATAATTTTGGAGCCAGTTAATTTTTTTCAGTATTTTGTGCTGTCCTTGGGAATGGGCCCTCAGAGGAC
AGTGCTTCCAAAGTACATCTTCTCCAGATCTCTGGCCCTTTTAAATGAGCTATTGTTAAACCAACAGGCTAGTTTATCTT
ACATCAGACCCCTTTTCTGGTAGAGGGGAAAATGTTTGTGCTTTTCCCTTTTCTTCTGTTAATACTTATGGTAAACACCTAAC
TGAGCCCTCACTCACATTAAATGATTCACTTGAAATATATACAGAAATTGTAAATTGTCTTTTTTTTAAAAAGGGGGCTAA
AGTAACACTTTTCTACTTATGTAAATTATAGATCCTAAATTCACGCACCCCGTGGGAGCTCAATAAAGATTTACTGAATT

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TCAACAGGGACGATTACGAGCTGCAGGAGGTGATCGGGAGTGGAGCAACTGCTGTAGTCCAAAGCAGCTTATTGTGCCCT
AAAAAGGAGAAAGTGGCAATCAAAACGGATAAACCTTGAGAAATGTCAAACTAGCATGGATGAACTCCTGAAAGAAATTCA
AGCCATGAGTCAATGCCATCATCCTAATAATTGTATCTTACTACACATCTTTTGTGGTAAAGATGAGCTGTGGCTTGTCA
TGAAAGCTGCTAAGTGGAGGTTCTGTCTGGATATTATTAAGCACATTTGTGGCAAAAGGGGAACACAAAAGT

60/76

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ATGGCGGACCTGGGGCTGGAGGGACAGGGAGGTACGGATCTGGGCCACCTGCGGGATCCAACTGGAATATTCTCACT
AGATAAAACCATTTGGCTTGGTACTTATGGCAGAACTCTATTGGGACTTCATGAGAAGACTGGTGCAATTIACAGCTGTTA
AAGTGATGAACGCTCGTAAGGATGAGGAAGAGGATCTCAGGACTGAACCTCAACCTTCTGAGGAAGTACTCTTCCACAAA
AACATTGTGTCTTCTATGGAGCATTTTTCAGCTGAGTCCCCCTGGTCAGCGGCACCACTTTGGATGGTGATGGAGTT
ATGTGCAGCAGGTTCCGGTCACTGATGTAGTGAGAAATGACCAGTAATCAGAGTTTAAAGAAGATTGGATTGCTTATATCT
GCCGAGAAAATCCTTCAGGGCTTAGCTCACCTTCACGCACACCCGAGTAATTCACCGGACATCAAAGTCAAGATGTGCTG
CTGACTCATAAATGCTGAAGTAAACTGGTTGATTTTGGAGTGAGTGCCTCAGGTGAGCAGAACTAATGGAAAGGAATAG
TTTCATTGGGACACCATACTGGATGGCACCTGAGGTGATTGACTGTGATGAGGACCCCAAGACGCTCCTATGATTACAGAA
GTGATGTGTGGTCTGTGGGAATTACTGCCATTGAAATGGCTGAAGGAGCCCCCTCTCTGTGTAACTTCAACCTTGGAA
GCTCTCTTCGTTATTTTGGGGAACTCTGCTCCACAGTCAAAATCCAGCGGATGGTCCCGTAAGTTCACAAATTCATGGA
AAAGTGACGATAAAAAATTTCTGTCTCTACTTCTGCAAAACATGCTTCAACACCCCAATTGTTCGGGATATAAAA

Fig. 11C

ATGAACGACATGTTGTTGAGTCATTAAACAAGGCATCTTACTGGAATCATTAATAAAGACAGAAAAGAACAGGCACGG
GAGAAAAATCAAAAGTTTCTACTCTGAGGCAAGCACTGGCAAAAAGACTATCACCAAAGAGGTTTCAGGGCAAAGTCATC
ATGGAGACCTGAAAAGCTTGAACTCTCGGATTTAGAAAGCCCGCAGGCAAGCGCCAAACGCAGATGGGAAGATATCTTTA
ATCAGCATGAGGAAGAATTGAGACAAAGTTGATAAAGACAAAGAAGATGAATCATCAGACAAATGATGAAGTATTTCAATTCG
ATTGAGGCTGAAGTCCAGATAGAGCCATTGGAAGCCATACATTTCAAATCCTAAAAAATTTGAGGTTCAAGAGAGATCTCC
TTCTGTGCCCTAACCAACAGGATCATGTCACATCATGTCAAGTTCTCTTCAAGCGTTCTCTCAGCGGTCCTTTTGGAAACAAG
CTCAGAAGCCCATTTGACATCAGACAAAGGAGTTGCAAAATCGTCAAAATTTGGCTGGCAGCATCAGGTGATTTCAAAGCAC
AAATTTTAGCAGGCAAAACACAGAGCTACTGTTTAAACAATTTATATTTCAAGAGTCAAGAAAGAAATTTCAAGAAGG
AATGAATCAAAAGTGTGAGGAGCCCAAGTAGGATTAGGACCTGAAGGCCATTGTATTTGGCAATTTGGGTGAATCTTCTT
CTGAGGAAGAAGTCTGTGACTGGAAGGAGGTCTCAGTCAATCACCACTTATTTCTACTATTGATCAGAAAGTTGCTGGTT
GACATCCATGTTCCAGATGGATTTAAAGTAGGAAAAATATCACCCCTGTATACCTTGACAAACGAATGGGTAGGCTATAA
TGCACTCTCTGAAATCTTCCGGAATGATTGGTTAACTCCGGCACCTGTCAATTCAGCCACCTGAAGAGGATGGTGATTATG
TTGAACCTCTATGATGCCAGTGTGATACCTGATGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CATGCCAATGGCAATGAT
TAAGTTTGTGAT
GCAAGCAAGATGGTTATGATGGAAGTCTGGAAAGAGGAGGCTACAGAGGCTATGGAGCCATACAGCCCAATAGAAAGC
CATGGAGGAAGTGCAGCCAGTGAGGACAAATGCAGCCATTGGAGATCAGGAAGACATGCAGCCCAATATAGGCAGTGAAAG
AAGAGGCAGTGAGGATGAGGAGTGGTTCGAACCAAGTGAAGAGAGTGAGGCCCTTGGACTCAATGGAGAG
AAAATTGCTCAGAGACAGATGTTCCAGGATTGAAGAGACCTGCGTCTCAGGACTTTGAATATCTACAGGAGGAGCCAGGT
GGTGGAAATGAGGCCCTCAAATGCCATTGACTCAGGTGCTGCACCGTCAACCTGATCATGAGAGTGACAAATAAGGACAT
ATCAGAAATCATCAACAAATCAGATTTTCTGCCAATCACTCATCTCTTCCAAAGTTCTGGGATGTCTGCTGATGCTA
ACTTTGCCAGTGCCCATCTTATACGCTGGATTCTGTAAGTACCTGAGGAATCACCTAAGCAACCTCTGAAAGTCAATGTT
AACCACCTCTATGCTCTCTGCAATGTAAAAAACCACTAATCCACATGTATGAAAAAGGAGTTCACTTCTGAGATCTGCTG
TGGTTCCTTTGTGGGGAGTCAATTTGCTGTGTGGGAACCCGATCTAATCTATATCTGATGGACAGAAAGTGGAAAGGCTGACA
TTACTAAACCTTATAAGGCGAAGACCATTTCCGCCAGATTCAAGTCTTAGAGCCCACTCAATTTGCTGATTACCATCTCAGGT

91/76

Fig. 11D

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CCGGAGTGTC CGCGGTGGTGGCGGTGCCAAGAGAGCTGAAGGAGGCGCGGAGGCTCCAGGCCGAGCAGTTAGGC
 CCGGAGCGACTGCGGCGCGAGCCGATGAGTAACCCGAAGCCCTAGAGGAGTGGTCACCTGCCTGAGGGCACTTCTGTG
 CCCACCAAGCATCAGACCAGGCCGACCGAGTCCCCGGCACCATGTTTGGGAAGAGGAAGCGGGTGAGATCTCCGCGC
 CGTCCAACTTCGAGCACCGCGTGCCACACGGGCTTCGACCAGCACGAGCAGAAATTACGGGGCTGCCCCAGTGGCAG
 AGCTGATCGAGGAGTCGGCTCGCCGGCCCCAAGCCCCTCGTGACCCCCGCTGCATCACCTCCATCCAGCCCCGGGCCCC
 CAAGACCATCGTGGGGGAGCAAGGTGCCAAAGATGGGGCCCCACGCTGCTGGAACGAGTTTGAGAAACATGTCGG
 TGACACGCTCCAACCTCCCTGCGGAGAGACAGCCCGCCCGCCGCTGCGCCAGGAAATGGGATGCCAGAGGAG
 CCGGCCACCA CGGCCAGAGGGGGCCCCAGGGAAAGGCAGCGAGGCCGTTCCGCCGTACAGCGAGCGGGTGCGCGG
 CAGTGGTGACAGGCGACGGGCGGGGCCAGAGAAGAGGCCCAAGTCTTCCAGGGAGGGCTCAGGGGTCCCCAGGAGTCTCT
 CCGGGGACAAACGCCCTCTCCGGGCTGATGTGGGCACCCCCAGCTGCTGGCTCGGGCAGTGGGGCGAAACTGGCA
 GGTGGCCGCCCTTTAACACCTACCCGAGGGCTGACACGGACCAACCATCCCCGGGTGCCAGGGGAGCCTCATGACGT
 GGGCCCCTAACGGGCCCATCAGCGGGGGGCGCTGGCCATCCCCCAGTCTCTCTCTCCCCGGCTTCCCAACCCGAGCCC

Fig. 11E

GAGGTGCCCCAGCCCTGGAGTGTCTGGGACCCACGCCTCAGAGCCCCAGCTGGCCCCCTCCAGCCTGCACCCCCCGCCGCC
CCTGCTGTTCCCTGGGCCCCCTGGCCCTCACACAGCGGGAGCCACAGCGAGTATCCCATGAGCAGTTCCGGGCTGC
CCTGCAGCTGGTGGACCCAGCGACCCCGCTCTACCTGGACAACCTCATCAAGATTGGCGAGGGCTCCACGGGCA
TCGTGTGCATCGCCACCGTGCGCAGCTCGGGCAAGCTGGTGGCCGTCAAGAAGATGGACCTGCGCAAGCAGCAGAGGGCGC
GAGCTGCTTTCAACGAGGTGGTAATCATGAGGGACTACACGACGAGAAATGTGGTGAGATGTACAACAGCTACCTGGT
GGGGACGAGCTCTGGGTGGTCAATGGAGTTCCTGGAAAGGAGCGCCCTCACCGACATCGTCAACCCACACAGGATGAACG
AGGAGCAGATCGCGCGCTGTGCCCTTGCAGTGCTGAGGCCCTGTGCGTCTCCACGCCAGGGCGTCAATCCACCGGGAC
ATCAAGAGCGACTCGATCCTGCTGACCCCATGATGGCAGGGTGAAGCTGTCAAGACTTGGGTCTCGGCCCAAGGTGAGCAA
GGAAGTCCCCGAAAGGAGTCTGGTCGGCACGCCCTACTGGATGGCCCCAGAGCTCATCTCCGCTTCCCTACGGGC
CAGAGGTAGACATCTGGTCGCTGGGGATAATGGTGAATGAGATGGTGGACGGAGAGCCCCCTACTTCAACGAGCCACCC
CTCAAAGCCATGAAGATGATTCTGGGACAACCTGCCACCCCGACTGAAGAACCTGCACAAAGGTGTGCGCCATCCCTGAAGGG
CTTCTCTGGACCGCTGCTGGTGCAGACCCCTGCCACGCGGCCACCGCAGCTGCTGAAGCACCCCATTCCTGGCCA
AGGCAGGGCCGCTGCCAGCATCGTGCCTCTCATGCGCCAGAACCCGACACAGATGAGGCCCCAGCGCCCTTCCCTCAACC
AAAGAGCCCCCGGGTCAACCCCGCCACTGAGGCCAGTAGGGGCCAGGCCCTCCCACTCTCCAGCCCCGGGAGATG
CTCCGCTGGCACACCTCTCTTGTGGGGTAGATGAGACCTACTAGAACCTCCAGTTTGTATCTCGTGACTTTTAG
AAAACACAGGGACTCGTGGAGCAAGCGAGGCTCCAGGACCCCACTCTGGGACAGGCCCTCCCACTGTTCTCT
GTCTCCAGGAAGGCGAGCGCCCTCCCATCACTGGAAGTCTGCACTGGGGTCTGGGGTGGAGAGAACACTAAGAGG
TGAACATGTATGAGTGTGTGCACGCGTGTGATGTGTGTGTGTGTGCAAGGTCCAGCCACCCCTCCAGC
CCGCAAGGGGTGTCTGGCGCTTGCCCTGACACCCAGCCCCCTCTCCCTGAGCCATTGTGGGGTCCGATCATGATGTC
CGAAGAGTGGCCCTTTCCCGTAGCCCTGCGCCCCCTTCTGTGGCTGGATGGGGAGACAGGTCAAGGCCCCCACTCT
CCAGCCCCCTGCAGCAATGACTACTGCACCTGGACAGCCCTCTCTTTCTAGAACTCTATTATATTGTCATTTTATAC
ACTCTAGCCCCCTGCCCCCTATTGGGGGACAGATGGTCCCTGTCCCTGGGGGTGGCCCCCTGGCAGAACCACTGCTGAAGAAC
CAGGTTCTCTGCCCCGTGAGCGCAGCCCCAGCCCCGCCCCCTGCTCGAGTTAGTTTACAATTAAACATTGTCTTGT
TTTGTG

63/76

Fig. 11F

64/76

Fig. 11G

GCAGCAAGTGGAGAAGATGGAGCAAGACCATGCCGTGCGCCGCGGAGGAGGCCAGGGCGGATCCGCCCTGGAGCAGGATC
GGGACTACACCAAGGTTCCAAGAGCAGCTCAAACTGATGAAGAAAGAGGTGAAGAACGAGGTGGAGAAAGCTCCCCGACAG
CAGCGGAAGGAAGCATGAAGCAGAAATGGAGGACACCGCAGAAAGCAGCTTCTTGACCCGGGACTTTGTAGCCAA
GCAGAAAGGAGGACCTGGAGCTGGCCATGAAGAGGCTCACCAACCGACAAACAGGCCGGGAGATCTGTGACAAAGGAGCGCGAGT
GCCTCATGAAGAACGAGGAGCTCCCTTCGAGACCCGGGAAGCAGCCCTGTGGGAGATGGAAAGAGCACCAAGCTGCAGGAGAGG
CACCAAGCTGGTGAAGCAGCAGCTCAAAGACCAGTACTTCCTCCAGCGGCACGAGCTGCTGCGCAAGCATGAGAAGGAGCG
GGAGCAGATGCAGCGCTACAACAGCGCATGATAGAGCAGCTGAAGGTGCGGCAGCAACAGGAAAGGCGCGGCTGCCCA
AGATCCAGAGGAGTGAGGGCAAGACGCGCATGGCCATGTACAAAGAGAGCTCCACATCAACGGCGGGGCGAGCGCAAGCT
GAGCAGCGTGAGAAGATCAAGCAGTTCTCCAGCAGGAGGAGAGGAGGCGGCTGCGAGCGGCTGCAGCAACAGCAGAA
ACACGAGAACCCAGATGCGGGACATGCTGGCGCAGTGCGGAGCAACATGAGCGAGCTGCAGCAGCTGCAGAAATGAAAAGT
GCCACCTCCTGCTAGACGACGAAACCCAGAACTGAAGGCCCTGGATGAGAGCCATAACCAAGAACTGAAGGAATGGCGG
GGACAAGCTTCGGGCCGCGCAAGAGGCTCTGGAAAGAGGATCTGAACCAAGAAAGCGGGAGCAGGAGATGTTCTTCAAGCT
GAGCGAGGAGGCGGAGTGCCCCAAACCCCTCCACCCCCAAGCAAGGCCCAAGTTCTTCCCCCTACAGCTCTGGGGATGCTT
CC

Fig. 11H

Fig. 12A

STLK6_h	L	S	P	E	L	L	R	Q	D	L	H	G	Y	N	V	K	S	D	I	Y	S	V	G	I	T	A	C	E	L	A	S	G	Q	V	P	F	Q	D	M	H	R	T	Q	M	L	L	Q	K	L	K	282																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
STLK5_h	L	S	P	E	V	L	Q	Q	N	L	Q	G	Y	D	A	K	S	D	I	Y	S	V	G	I	T	A	C	E	L	A	N	G	H	V	P	F	K	D	M	P	A	T	Q	M	L	L	E	K	L	N	200																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
SPAK_h	M	A	P	E	V	M	E	Q	-	V	R	G	Y	D	F	K	A	D	M	W	S	F	G	I	T	A	I	E	L	A	T	G	A	A	P	Y	H	K	Y	P	P	M	K	V	L	M	L	T	L	Q	289																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
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SPAK_h	N	D	P	P	T	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

Fig. 12B

PAK1_h U51120	MSNNGLDIQDKPPAPPMRNTSTMIGAGSKDAGTLNHGSKPLPPNPEEKKKKDRFYRSILP	60
PAK4_h	-----	0
PAK5_h	-----	0
PAK1_h U51120	GDKTNKKKEKERPEISLPSDFEHTIHVGFDVAVT-GEFTGMPPEQWARL LQTSTNITKIS	115
PAK4_h	---MFRKKKKRPEISAPQNFQHRVHTSFDPKEGKFVGLPPQWQNILD-ILRRPKPVVDP	56
PAK5_h	---MF-GKRKKRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWQSLIEESARRPKPLVDP	56
PAK1_h U51120	-----	115
PAK4_h	SRITRVQLQPMKTVVRGSAAMPVDGYISGLLNDITQKLSVISNTLRGRSPTSRRRAQSLGL	116
PAK5_h	ACITSIQPGAPKTIIVRGSKGAKDGA LTL LLLDEFENMSVTRSNGLRRDSPPPARAR	112
PAK1_h U51120	-----	115
PAK4_h	LGDEHWATDPDMYLQSPQSERTDPHGLYLSGNGTTPAGHKQMPWPEPQSPRVLPNGLIAAK	176
PAK5_h	-----QENGMPPEEPATTIARGGPGK	131
PAK1_h U51120	-----	127
PAK4_h	AQSLGPAEFQGA SQRCLQLGAC LQSSPPGASPTGTNRHGMKA AKHGSEEARPQSC LVGS	236
PAK5_h	AGSRGR-----FAGHS EAGGSGDRRRAAGPEKRPKSSREGSGGPQESSRD KRP-----LSGP	183
PAK1_h U51120	LEFY-NSKKTSNSQKYMISFTDKS-----AEDYNSSNALNVKA-----VSETPAVPPVS	174
PAK4_h	ATGRPGGEGSPSPK TRESSLKRLFRSMFLSTAAATAPSSSKPKGPPPPQSKPNSSFRPPQK	296
PAK5_h	DVGTPTQPAGLASGAKLAAG-----RPFNTYPRADTDHP SRGAQGEPHDVA PNGP-----	232


Fig. 13A

PAK1_h U51120	E	E	D	E	D	D	D	D	D	A	T	P	P	P	V	I	A	P	R	P	E	H	T	K	S	V	T	R	S	-	-	-	V	I	E	P	L	P	V	T	P	T	R	D	V	A	T	S	P	I	S	P	T	E	N	N	T	T	230		
PAK4_h	D	N	P	P	S	L	V	A	K	A	Q	S	L	P	S	D	Q	P	V	G	T	F	S	P	L	T	T	S	D	T	S	S	P	Q	K	S	L	R	T	A	P	A	T	G	Q	L	P	G	R	S	S	P	A	G	S	P	R	T	W	H	356
PAK5_h	-	-	-	-	-	-	-	-	-	-	-	S	A	G	G	L	A	I	P	O	S	S	S	S	S	S	S	S	S	S	S	R	P	T	R	A	R	G	A	P	S	P	G	V	L	-	-	-	-	-	G	P	H	A	S	E	268				
PAK1_h U51120	P	-	-	-	-	-	-	-	-	-	-	P	D	A	L	T	L	N	T	E	K	Q	K	K	P	K	M	S	D	E	E	I	L	E	K	L	R	S	I	V	S	V	G	D	P	K	K	K	Y	T	R	F	E	K	I	276					
PAK4_h	A	Q	I	S	T	S	N	L	Y	L	P	Q	D	P	T	V	A	K	G	A	-	-	-	L	A	G	E	D	T	G	V	V	T	H	E	Q	F	K	A	A	L	R	M	V	V	D	Q	G	D	P	R	L	L	D	S	Y	V	K	I	413	
PAK5_h	P	Q	L	A	P	P	A	-	C	T	P	A	A	P	A	V	P	G	P	R	S	P	Q	R	E	P	Q	R	V	S	H	E	Q	F	R	A	A	L	Q	L	V	V	D	P	G	D	P	R	S	Y	L	D	N	F	I	K	I	327			
PAK1_h U51120	G	Q	G	A	S	G	T	V	Y	T	A	M	D	V	A	T	G	Q	E	V	A	I	K	M	N	L	Q	Q	Q	P	K	K	E	L	I	T	N	E	I	L	V	M	R	E	N	K	N	P	N	I	V	N	Y	L	D	S	Y	L	V	336	
PAK4_h	G	E	G	S	T	G	I	V	C	L	A	R	E	K	H	S	G	R	Q	V	A	V	K	M	M	D	L	R	K	Q	R	R	E	L	L	F	N	E	V	V	I	M	R	D	Y	Q	H	E	N	V	V	E	M	Y	K	S	Y	L	V	473	
PAK5_h	G	E	G	S	T	G	I	V	C	I	A	T	V	R	S	S	G	K	L	V	A	V	K	K	M	D	L	R	K	Q	R	R	E	L	L	F	N	E	V	V	I	M	R	D	Y	Q	H	E	N	V	V	E	M	Y	N	S	Y	L	V	387	
PAK1_h U51120	G	D	E	L	W	V	V	M	E	Y	L	A	G	G	S	L	T	D	V	V	T	E	I	C	M	D	E	G	Q	I	A	A	V	C	R	E	C	L	Q	A	L	E	S	L	H	S	N	Q	V	I	H	R	D	I	K	S	D	N	I	L	396
PAK4_h	G	E	E	L	W	V	L	M	E	F	L	Q	G	G	A	L	T	D	I	V	S	Q	V	R	L	N	E	E	Q	I	A	T	V	C	E	A	V	L	Q	A	L	A	Y	L	H	A	Q	G	V	I	H	R	D	I	K	S	D	S	I	L	533
PAK5_h	G	D	E	L	W	V	V	M	E	F	L	E	G	G	A	L	T	D	I	V	T	H	T	R	M	N	E	E	Q	I	A	A	V	C	L	A	V	L	Q	A	L	S	V	L	H	A	Q	G	V	I	H	R	D	I	K	S	D	S	I	L	447
PAK1_h U51120	L	G	M	D	G	S	V	K	L	T	D	F	G	F	C	A	Q	I	T	P	E	Q	S	K	R	S	T	M	V	G	T	P	Y	W	M	A	P	E	V	V	T	R	K	A	Y	G	P	K	V	D	I	W	S	L	G	I	M	A	I	E	456
PAK4_h	L	T	L	D	G	R	V	K	L	S	D	F	G	F	C	A	Q	I	S	K	D	V	P	K	R	K	S	L	V	G	T	P	Y	W	M	A	P	E	V	I	S	R	S	L	Y	A	T	E	V	D	I	W	S	L	G	I	M	V	I	E	593
PAK5_h	L	T	H	D	G	R	V	K	L	S	D	F	G	F	C	A	Q	V	S	K	E	V	P	R	R	K	S	L	V	G	T	P	Y	W	M	A	P	E	L	I	S	R	L	P	Y	G	P	E	V	D	I	W	S	L	G	I	M	V	I	E	507
PAK1_h U51120	M	I	E	G	E	P	P	Y	L	N	E	N	P	L	R	A	L	Y	L	I	A	T	N	G	T	P	E	L	Q	N	P	E	K	L	S	A	I	F	R	D	F	L	N	R	C	L	E	M	D	V	E	K	R	G	S	A	K	E	L	L	516
PAK4_h	M	V	D	G	E	P	P	Y	F	S	D	S	P	V	Q	A	M	K	R	L	R	D	S	P	P	K	L	K	N	S	H	K	V	S	P	V	L	R	D	F	L	E	R	M	L	V	R	D	P	Q	E	R	A	T	A	Q	E	L	L	653	
PAK5_h	M	V	D	G	E	P	P	Y	F	N	E	P	L	K	A	M	K	M	I	R	D	N	L	P	P	R	L	K	N	L	H	K	V	S	P	S	L	K	G	F	L	D	R	L	L	V	R	D	P	A	Q	R	A	T	A	A	E	L	L	567	

Fig. 13B

545
 681
 591

PAK1_h	U51120	Q	H	Q	F	L	K	I	A	K	P	L	S	L	T	P	L	I	A	A	K	E	A	T	K	N	N	H
PAK4_h		D	H	P	F	L	L	Q	T	G	L	P	E	C	L	V	P	L	I	Q	L	Y	R	K	Q	T	S	T
PAK5_h		K	H	P	F	L	A	K	A	G	P	P	A	S	T	I	V	P	L	M	R	Q	N	R	T	R		

 RESIDUES THAT MATCH THE CONSENSUS NAMED CONSENSUS #1 EXACTLY.


 BOX RESIDUES THAT MATCH THE CONSENSUS EXACTLY.

Fig. 13C

ZC4_h.pro	MAGPGGWRDREVTDLGHLPDPTGIFSLDKTIIGLTYGRIYLGHEKGTGAF	50
ZC1_h.pro	MANDSPAKSLVDIDLSSLRDPAGIFELVEVVGNGTYGQVYKGRHVKTGQL	50
ZC4_h.pro	TAVKVMNARKDEEEDLRTLENLRLKYSFHKNIVSFYGAFFKLSPPGQRHQ	100
ZC1_h.pro	AAIKVMDVTEDEEEEIKLEINMLKKYSHHRNIAITYYGAFTKKSPPGHDDQ	100
ZC4_h.pro	LWMVMELCAAGSVTDVVRMTSNOSLKEDWIAIYICREILQGLAHLHAHRVI	150
ZC1_h.pro	LWLVMEFCGAGSITDLVKNTKGNLTKEDWIAIYSREILRGLAHLHIHVI	150
ZC4_h.pro	HRDIKGQNVLLTHNAEVKLVDFGVSAQVSRITNGRRNSFIGTPYWWMAPEVI	200
ZC1_h.pro	HRDIKGQNVLLTEINA EVKLVDFGVSAQLDRTVGRRTFIGTPYWWMAPEVI	200
ZC4_h.pro	DCDEDPRRSYDYRSDVWSVGITAIEMAEGAPPLCNLQPLEALFVILRESA	250
ZC1_h.pro	ACDENPDATYDYRSDLWSGIGITAIEMAEGAPPLCDMHPMRALEFLIPRNPP	250
ZC4_h.pro	PTVKSSGWSRKFFHNFMEKCTIKNLFERPTSANMLQHPFVRDIKNERHVVE	300
ZC1_h.pro	PRLKSKKWSKKFFSFIIEGCLVKNYMQRPSTEQLKHPEIRDPNERQVRI	300
ZC4_h.pro	SLTRHLTGIKKR-----QKKEQAREKKS	324
ZC1_h.pro	QLKDHIDRTRKRRGEKDETEYEYSGSEEEEEVEPEGEPESSIVNVPGES	350
ZC4_h.pro	KVSTLRQALAKRLSPKRRFRAKSSWRPEKLELSDLEARRQRRQRWEDIFN	374
ZC1_h.pro	TLRDFLRLLQENKERSEALRRQQLLQEQQLREQEYKRQLLAERQKRIE	400
ZC4_h.pro	QHEEELRQVDKDEDESSDNDEVFHSIQAEVQIEPLKPYISNPKKIEVQE	424
ZC1_h.pro	QQKEQRRLLEEQQRREREARRQQREREQRRREQEIEKRRLEELERRRKEEEE	450

Fig. 14A

ZC4_h.pro	RSPV	NNQD	HAHV	KFSS	VPQR	SLLE	QAQK	PIDIR	QRSS	QNRQ	NWLAA	474
ZC1_h.pro	RRRA	EEKRR	VERE	QEYI	RRQL	EEEE	QRHL	EVLL	QQQL	QEQAM	LLECR	500
ZC4_h.pro	SGDS	KKIL	AGKT	QSYC	LTIY	ISEV	KKKE	EFQE	GMNQ	KCQA	QVGL	524
ZC1_h.pro	MEEH	RQAER	LQRQ	LQEQ	AYLL	SLQH	DHRR	PHPH	QHSQ	QPPQ	QERS	550
ZC4_h.pro	CIWQ	LGE	SSSE	EE	SPVT	GRRS	QSSP	PYST	IDQK	LLVD	IHPD	574
ZC1_h.pro	FHAPE	KAHYE	PADRA	REVE	DRFR	KTNH	SSPE	AQSK	QTGR	VLEPP	PSRS	600
ZC4_h.pro	PPVY	LTNW	VGYN	ALSE	IFRN	DWLT	PAPV	IOPP	EEDG	DYVEL	YDAS	624
ZC1_h.pro	ESFS	NGN	SESV	HPAL	LQRP	AEQV	PVRT	TSRSP	VLSRR	DSP	LQGS	650
ZC4_h.pro	GDD	DES	NDT	FEDT	YDH	ANG	DDLD	NQVD	QAND	VCKD	HDDN	674
ZC1_h.pro	AGQR	NSTS	IEPR	LLWE	RVK	LVRP	GS	SSGS	SSNS	GSQ	SGSG	700
ZC4_h.pro	NNY	EAP	SCPR	ASYG	RDG	SC	KQD	GYD	GSRG	KEE	AYRG	724
ZC1_h.pro	GERF	RVR	SSK	SEGS	PSQR	LEN	AVKK	PEDK	KEV	FRPL	KPAD	750
ZC4_h.pro	AASE	DNA	AI	GDQ	EEHA	ANIG	SERR	GS	EGDG	GKGV	RTSE	774
ZC1_h.pro	AVED	VRP	PHK	VTD	YSS	SEES	GTTD	EE	DD	DVE	QEG	800
ZC4_h.pro	NCSE	TDGP	GLKR	PA	SQD	FEY	LQEE	PPGG	GNEA	SN	AI	824
ZC1_h.pro	SLNL	SN	GET	SVK	TMIV	DDVE	SE	PIAM	TPS	KEGT	LI	850
ZC4_h.pro	KDI	SE	ST	OSD	FS	AN	HS	SPSK	SG	SG	MS	874
ZC1_h.pro	KSS	SS	S	F	T	P	F	I	D	PR	LL	898

Fig. 14B

ZC4_h.pro	PSEVNVNPLYVSPACKKPLIHMYEKEFTSEICCGSLWGVNLLLGTRSNLY	924
ZC1_h.pro	GSVNVNPTNTRPIQSPTPEIRKRYKKRFFNSEILCAALWGVNLLVGTESGLM	948
ZC4_h.pro	LMDRSGKADITKLIIRRRPFRQIQVLEPLNLLITISGHKNRRLRVYHLLTWLR	974
ZC1_h.pro	LLDRSGQGKVPYPLINRRRFQQMDVLEGLNVLLVTISGKKDKLIRVYYLSWLR	998
ZC4_h.pro	NKILNNDPESKRRQE-EMLKTEEACKAIDKLTGCEHFSVLQHEETIYIAI	1023
ZC1_h.pro	NKILHNDPEVEKKQGT-----TVGDLEGCVHYKVVKYERIKFLVI	1039
ZC4_h.pro	ALKSSIHLAWAPKSFDESTAIKVFPITLDHKPVTVDLAIGSEKRLKIFFS	1073
ZC1_h.pro	ALKSSVEVYAWAPKPYHKFMAFKSFGEVLVHKPLLVDLTVEEGQRLKVIYG	1089
ZC4_h.pro	SADGYHLIDAESVMSDVTLPKNPLEIIPQNIILPDCLGIGMMLTFNAI	1123
ZC1_h.pro	SACGFHAVDVDSGSVYDIYLPTHIQCSIKPHAIILPNTDGMELLVCYED	1139
ZC4_h.pro	EALSVANEQLFKKILEMWKDIPISSIAFECTORITGWGOKAIEVRSLQSR	1173
ZC1_h.pro	EGVYVNTYGRITKDVVLQWGEPTSVAYIRSNQIMGWGEKAIETIRSVETG	1189
ZC4_h.pro	VLESELKRRSIIKLRFLCTRGDKLFESTLRNHHSRVYFMTLGKLEELQS	1223
ZC1_h.pro	HLDGVFMHKRAQRLLKFLCERNDKVFFASVRSGGSSQVYFMTLGRTSLLSW	1239
ZC4_h.pro	NYDV	1227
ZC1_h.pro		1239

BOX RESIDUES THAT MATCH ZC4_h.pro EXACTLY.

Fig. 14C

Db = LOK1_m

Qy = GEK2_h

Db 1 MAFANFRRI LSTFEKRKSREYEHVRRDLDPNDVWEIVGELGDGAFGKVKYKAKNKETGA 60
Qy 1 MAFANFRRI LSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVKYKAKNKETGA 60

Db 61 LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYDGGKLVIMIEFCPPGGAVDA 120
Qy 61 LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYHDGKLVIMIEFCPPGGAVDA 120

Db 121 IMLELDRGLTEPQIQVVCRCQMLEALNFLHGKRRIIHRDLKAGNVLMTLEGDIRLADFGVSA 180
Qy 121 IMLELDRGLTEPQIQVVCRCQMLEALNFLHRSKRRIIHRDLKAGNVLMTLEGDIRLADFGVSA 180

Db 181 KNLKTLQKRDSFIGTPYWMapevVLCETMKDAPYDYKADIWSLGITLIEMAQIEPPHHEL 240
Qy 181 KNLKTLQKRDSFIGTPYWMapevVLCETMKDTPDYKADIWSLGITLIEMAQIEPPHHEL 240

Db 241 NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLQHPFVSRVTSN 300
Qy 241 NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLEHPFVSSITSN 300

Db 301 KALRELVAEAKAEVMEEIEDGREDEGEEDAVDAPPLVNHTQDSANVTQPSLDSNKLQD 360
Qy 301 KALRELVAEAKAEVMEEIEDGREDEGEEDAVDAASTLENHTQNSSEVSPPSLNADKPLEE 360

Fig. 15A

* * * * *
Db 361 S-STPLPPSQPEPVNGPCSPSGDGPLQTTSPADGLSKNDNDLKVPVPLRKSRPLSMDA 419
Qy 361 SPSTPLAPSQSQDSVNEPCSPSGDRSLQTTSPVAVPGNENGLAVPVPLRKSRPVSMMDA 420

* * * * *
Db 420 RIQMDEEKQIPDQDENPSPAASKSQKANQSRPNSSALETLGGEALTNGGLELPSSVTPSH 479
Qy 421 RIQVAQEKQVAEQGGDLSPAANRSQKASQSRPNSSALETLGGEKLANGSLEPPAQAAAPGP 480

* * * * *
Db 480 SKRASDCSNLSTSESM DYGTSLADLSLNKETGSLSLKGSKLHNKTLKRTRRFVVDGVEV 539
Qy 481 SKRSDCSSLCTSESM DYGTNLSTDLSLNKEMGSLSIKDPKLYKTKLKRTRKFVVDGVEV 540

* * * * *
Db 540 SITTSKIISEDEKKDEEMRFLRRQELRELRLQLKKEEHRNQTQLSSKHLEQLQEMHKRFEQ 599
Qy 541 SITTSKIISEDEKKDEEMRFLRRQELRELRLQLKKEEHRNQTQLSNKHLEQLQEMHKRFEQ 600

* * * * *
Db 600 EINAKKKFYDVELENLERQKQKQVEKMEQDHSVRRKEEAKRIRLEQDRDYAKFQEQLKQM 659
Qy 601 EINAKKKFFDTELENLERQKQKQVEKMEQDHA VRRRREEARRIRLEQDRDYTRFQEQLKLM 660

* * * * *
Db 660 KKEVKSEVEKLPRQQRKESMKQKMEEHSQKKQLDRDFVAKQKEDLELAMRKLTTENRRE 719
Qy 661 KKEVKNEVEKLPRQQRKESMKQKMEEHTQKKQLDRDFVAKQKEDLELAMKRLTTDNRRRE 720

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*****
Db 720 ICDKERDCLSKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHDLRLKKHEKE 779
Qy 721 ICDKERECLMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHELRLKKHEKE 780

*****
Db 780 REQMQRYNQRMMEQLKVRQQQEKAARLPKIQRS DGETRMAMYKKS LHINGAGSASEQREKI 839
Qy 781 REQMQRYNQRMIEQLKVRQQQEKAARLPKIQRS EGKTRMAMYKKS LHINGGSAAEQREKI 840

*****
Db 840 KQFSQQ'E EKQRQKAERLQQQKKHEHQMRDMVAQCESNMSELQQQLQNEKCYLLVEHETQKLK 899
Qy 841 KQFSQQ'E EKQRQKSERLQQQKKHENQMRDMLAQCESNMSELQQQLQNEKCHLLVEHETQKLK 900

*****
Db 900 ALDESHNQSLKEWRDKLRPRKKALEEDLNQKKREQEMFFKLSEEA E-PRPTTPSKASNFF 958
Qy 901 ALDESHNQNLKEWRDKLRPRKKALEEDLNQKKREQEMFFKLSEEA ECPNPSTPSKAAKFF 960

*****
Db 959 PYSSGDAS 966
Qy 961 PYSSGDAS 968
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Fig. 15C